

SEQUENCE LISTING

<110> MEINKE, ANDREAS
MIN BUI, DUC
NAGY, ESZTER

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<140> 2005-09-30

<150> PCT/EP2004/003398

<151> 2004-03-31

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<170> PatentIn version 3.1

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<211> 1287

<212> DNA

<213> Staphylococcus epidermidis

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<212> DNA

<213> Staphylococcus epidermidis

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<211> 2676

<212> DNA

<213> Staphylococcus epidermidis

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<212> DNA

<213> Staphylococcus epidermidis

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<211> 888

<212> DNA

<213> Staphylococcus epidermidis

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 <213> Staphylococcus epidermidis

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 ggatatcaat tacctcaatc taagattcaa acacgttcca ttcatagtga agatattaca 1080

ggtaacgaat cacatatatt agatgtacgt aatgataatg aatggaataa tggccactta	1140
tctcaagcgg ttcattgtacc acacggcaaa ctttttagaaa cagatttacc tttcaataga	1200
aacgatgtta tttatgtaca ctgtcagtct ggcattagaa gttcgatagc tattggtatt	1260
ttagaacata aagggttatca caacattatt aatgtaaattg aagggttaca agatatacac	1320
ctttct	1326

<210> 26
 <211> 855
 <212> DNA
 <213> Staphylococcus epidermidis

<400> 26	
ttgaaaaaaa ttctggtggt aagtttaacg gcatttttag ttttggtctg ttgtaattca	60
ggtgataaga ctgatactaa agataagaaa gaagaaacaa agcaaacttc aaaggcaaat	120
aaagagaaca aagaacaaca tcataagcaa gagaatgata ataaggcttc aactcaattg	180
tcagaaaaag aaagggttagc attagcattt tatgcggatg gagtagaaaa atatatgtta	240
actaaaaacg aagtgttgac aggcgtgtat gattatcaaa aaggaaatga aacagagaag	300
aaacaaatgg aacaattgat gttagaaaaa gctgattcga tgaaaaatgc gccaaaggat	360
atgaaatttt atcaagttta tccgtctaaa ggacagttcg cttcaattgt tgggtgtaaat	420
aaaaataaaa tattttatagg tagtacgcaa ggcgcactga ttgattatca aacattatta	480
aataatggca aggagttaga tattagtcaa ttgtatgaag ataataaaga caatcgctca	540
ttggaagaaa tgaagaataa aatagagatt gttgatagtg gagcagctca aaaagctgat	600
gacctgata aaaattctgc aaatacgatg gcacatatga gaagtcaaatt ttatgaaaaa	660
ataagtgact ttgatggtaa gttagataat aaaacttatc tatgggacaa tattagaatc	720
aatgacgatg gtaattggac agttcattac cgtaatcatg atggtgaaat tatgggtact	780
tataagagtg agaaaaataa aattattaaa cttgatcaaa atggaaataa aattaaagaa	840
caacaaatgt ctaat	855

<210> 27
 <211> 1494
 <212> DNA
 <213> Staphylococcus epidermidis

<400> 27	
atggctaata aagagtcaaa aaatgttggt attattggcg ctggtgtctt aagtacgaca	60
tttggttcta tgattaaaga attagaacct gattggaaca tcaaactcta tgaacgctta	120
gacgtccag gtattgaaag ttctaacgaa agaaacaatg ccggtacagg acatgcggcg	180
ttatgtgaat tgaactatac agtacaacaa cctgatgggt caattgatat agaaaaagcc	240

aaagaaatca	acgaacaatt	cgagattttca	aaacaatttct	ggggtcactt	agtaaaaaagt	300
ggtaacatca	gtaaccctag	agattttcatt	aatccacttc	ctcacattag	tttcgtaaga	360
ggtaaaaaata	acgttaaatt	cttaaaaaaac	cgttacgaag	caatgcgtaa	cttcacctatg	420
ttcgataaca	tcgaatatac	agaagatatc	gaagaaatga	gaaaatggat	gccattaatg	480
atgacaggtc	gtactggtaa	cgaaatcatg	gcggttagta	aaatcgacga	aggtacagat	540
gttaactacg	gtgaattaac	tcgtaaaatg	gcaaaaagta	ttgaaaaaca	tccaaagtgt	600
gatgttcaat	acaaccacga	agtaattaat	ttcaatcgtc	gtaaagacgg	tatttgggaa	660
gttaaagtta	aaaaccgtaa	ttctggagac	gttgaaactg	ttctagctga	ttatgtattt	720
atcggtgcag	gcggtggcgc	tattccacta	ttacaaaaaa	ctggtatccc	agaaagtaaa	780
catcttggtg	gattccctat	cagtggtcag	ttcttaattt	gtacaaacc	tgatgtaatt	840
aatgaacatg	acgtcaaagt	atatggtaaa	gaaccaccag	gcacacctcc	aatgactgta	900
ccacatttag	atacacgtta	tatcgatggg	gaaagaacat	tattatttgg	accatttgca	960
aatattggcc	ctaaattctt	aagaaacggg	tctaacttag	acttattcaa	atcagttaaa	1020
ccttataaca	tcacaacatt	actagcatct	gcagttaaaa	acttaccttt	aatcaaatac	1080
tctatcgacc	aagtattaat	gactaaagaa	ggttgtatga	accatctacg	cacgttctac	1140
cctgaagctc	gtgacgaaga	ttggcaatta	tacactgcag	gtaaacgtgt	tcaagttatc	1200
aaagatacta	aagaacacgg	taaaggattc	attcaatttg	gtacagaagt	tggttaactct	1260
aaagaccact	ctgttatcgc	actattgggt	gaatcacctg	gagcatcaac	ttcagtatca	1320
gtagccctag	aagttttaga	gaaaaacttt	gctgagtatg	aaaaagattg	gactccaaaa	1380
ttacaaaaaa	tgatcccatc	atatggtaaa	tctcttatcg	atgatgttaa	gttaatgaga	1440
gcaactcgta	aacaaacatc	taaagattta	gaattaaatt	attacgaatc	taaa	1494

<210> 28

<211> 1548

<212> DNA

<213> Staphylococcus epidermidis

<400> 28

atgaaaatat	ttaaaacttt	aagttctata	ctagttacat	ctgttctttc	tgtgactgtg	60
attccctcaa	catttgcac	aacagaatct	actgctacaa	atcagacaca	acaaacagta	120
ctttttgata	attctcatgc	tcaaactgcg	ggcgctgccg	attgggtgat	tgatggcgct	180
ttctcagatt	atgcagattc	aatgagaaag	caagggttacc	aagttaaaga	actagaagga	240
gaatcaaaca	tttctgatca	atctttacag	caggcgcatg	tattagttat	ccccgaagct	300
aacaatccat	ttaaagaaaa	tgagcagaaa	gcaatcatta	attttgttaa	aaatgggtgg	360

agcgtcattt	tcattctcaga	ccattataat	gccgatcgta	atttaaatacg	tattgattct	420
tcagaatcaa	tgaatgggta	tcgacgtggc	gcatacgaaa	atatgactaa	agatatgaat	480
aatgaagaaa	agaattctaa	cgttatgcat	aacgttaaga	gttctgattg	gctctcacia	540
aacttcgggtg	ttcgcttttag	atataatgca	cttgaggata	tcaataactca	aaatatcggt	600
tcaagcaaag	atagtttttg	tattactaaa	gggtgtacaat	cagtttcgat	gcacgcaggt	660
tcaacattag	caataactga	tcctaataaa	gctaaaggca	ttatttatat	gccggaacat	720
ttaacgcata	gtcaaaaatg	gcctcacgca	ggtgatcaag	gtatttacaa	tgggggtggc	780
atcaacgaag	gaccttatgt	agccatttca	aaaatcggca	aaggtaaagc	tgcattttatt	840
ggcgatagct	ccctcgtaga	agatcggtca	cctaaatatc	ttcgtgaaga	taatgggaaa	900
cctaaaaaaaa	cgtacgatgg	ttttaagaa	caagataatg	gaaagttatt	aaataattta	960
acaacatggc	taggcaaaaa	agaatctcaa	tcttctatga	aagacatggg	gattaaactt	1020
gataataaaa	caccgctact	taactttgag	caacctgaga	attcaattga	acctcaaaaa	1080
gaaccgtgga	ctaaccat	agaaggttac	aaatgggtatg	atcggtcaac	atttaaaaca	1140
ggtagtattg	gaagtaatca	acgggggtgct	gacgatggag	tagatgacaa	aagctcttct	1200
catcaaaaatc	aaaatgccaa	agttgaatta	actttacctc	aaaatatcca	accgcatcat	1260
ccatttcaat	ttacaatcaa	actcacggga	tatgagccta	atagcacaat	tagcgatgta	1320
agagttggac	tttataaaga	tggaggtaag	caaatcggta	gcttttcttc	taaccgtaac	1380
caattcaata	ctctcggcta	tagtcctggc	caatcaatta	aagcaaattg	tgcggggtgaa	1440
gcttcattca	cactcacagc	taaagtgaca	gatgaaatta	aagatgctaa	tattcgtggt	1500
aaacaaggga	aaaaaattct	attaactcaa	aaaatgaatg	aaaatttt		1548

<210> 29
 <211> 252
 <212> DNA
 <213> Staphylococcus epidermidis

<400> 29	
ggtacacccat	tagaattagt
ttttgtcaat	actttaggac
ctaaaccttg	tttcgctaaa
60	
ccaaataaaa	ttctactatt
agaatatatt	ccgctatttg
ttgcagatgc	tgctgctggt
120	
aaaacaacaa	aattaactat
gccagcagca	aagggaacac
caattagtgt	gaataattta
180	
acaaacggac	tactatcagg
atcaacttta	aaccatggaa
tgacagacat	gattacaagt
240	
aaaccaccta	ta
252	

<210> 30
 <211> 162

<212> DNA
 <213> Staphylococcus epidermidis

<400> 30
 tcatcggttaa gtaccataat tcctttttct ttaggagcat taggcaaatt taattctttc 60
 attgagcaaa tcataccact agaatctacc ccacgtaatt gggcatcttt aattaccatt 120
 ccgcttgga taacggcccc aacttttgca acaacgacct tc 162

<210> 31
 <211> 348
 <212> DNA
 <213> Staphylococcus aureus

<400> 31
 atgaaattta aaaaatatat attaacagga acattagcat tactttttatc atcaactggg 60
 atagcaacta tagaaggga taaagcagat gcaagtagtc tggacaaata tttaactgaa 120
 agtcagtttc atgataaacg catagcagaa gaattaagaa ctttacttaa caaatcgaat 180
 gtatatgcat tagctgcagg aagcttaaat ccatattata aacgtacgat tatgatgaat 240
 gaatatagag ctaaagcggc acttaagaaa aatgatttcg tatcaatggc tgatgctaaa 300
 gttgcattag aaaaaatata caaagaaatt gatgaaatta taaataga 348

<210> 32
 <211> 676
 <212> PRT
 <213> Staphylococcus epidermidis

<400> 32

Met	Lys	Arg	Thr	Asp	Lys	Ile	Gly	Val	Tyr	Leu	Lys	Leu	Ser	Cys	Ser
1				5					10					15	
Ala	Leu	Leu	Leu	Ser	Gly	Ser	Leu	Val	Gly	Tyr	Gly	Phe	Thr	Lys	Asp
			20					25						30	
Ala	Phe	Ala	Asp	Ser	Glu	Ser	Thr	Ser	Ser	Asn	Val	Glu	Asn	Thr	Ser
		35					40					45			
Asn	Ser	Asn	Ser	Ile	Ala	Asp	Lys	Ile	Gln	Gln	Ala	Lys	Asp	Asp	Ile
	50					55					60				
Lys	Asp	Leu	Lys	Glu	Leu	Ser	Asp	Ala	Asp	Ile	Lys	Ser	Phe	Glu	Glu
65					70					75				80	
Arg	Leu	Asp	Lys	Val	Asp	Asn	Gln	Ser	Ser	Ile	Asp	Arg	Ile	Ile	Asn
				85					90					95	

Asp Ala Lys Asp Lys Asn Asn His Leu Lys Ser Thr Asp Ser Ser Ala
100 105 110

Thr Ser Ser Lys Thr Glu Asp Asp Asp Thr Ser Glu Lys Asp Asn Asp
115 120 125

Asp Met Thr Lys Asp Leu Asp Lys Ile Leu Ser Asp Leu Asp Ser Ile
130 135 140

Ala Lys Asn Val Asp Asn Arg Gln Gln Gly Glu Glu Arg Ala Ser Lys
145 150 155 160

Pro Ser Asp Ser Thr Thr Asp Glu Lys Asp Asp Ser Asn Asn Lys Val
165 170 175

His Asp Thr Asn Ala Ser Thr Arg Asn Ala Thr Thr Asp Asp Ser Glu
180 185 190

Glu Ser Val Ile Asp Lys Leu Asp Lys Ile Gln Gln Asp Phe Lys Ser
195 200 205

Asp Ser Asn Asn Asn Pro Ser Glu Gln Ser Asp Gln Gln Ala Ser Pro
210 215 220

Ser Asn Lys Thr Glu Asn Asn Lys Glu Glu Ser Ser Thr Thr Thr Asn
225 230 235 240

Gln Ser Asp Ser Asp Ser Lys Asp Asp Lys Ser Asn Asp Gly His Arg
245 250 255

Ser Thr Leu Glu Arg Ile Ala Ser Asp Thr Asp Gln Ile Arg Asp Ser
260 265 270

Lys Asp Gln His Val Thr Asp Glu Lys Gln Asp Ile Gln Ala Ile Thr
275 280 285

Arg Ser Leu Gln Gly Ser Asp Lys Ile Glu Lys Ala Leu Ala Lys Val
290 295 300

Gln Ser Asp Asn Gln Ser Leu Asp Ser Asn Tyr Ile Asn Asn Lys Leu
305 310 315 320

Met Asn Leu Arg Ser Leu Asp Thr Lys Val Glu Asp Asn Asn Thr Leu
325 330 335

Ser Asp Asp Lys Lys Gln Ala Leu Lys Gln Glu Ile Asp Lys Thr Lys

340	345	350
Gln Ser Ile Asp Arg Gln Arg Asn Ile Ile Ile Asp Gln Leu Asn Gly		
355	360	365
Ala Ser Asn Lys Lys Gln Ala Thr Glu Asp Ile Leu Asn Ser Val Phe		
370	375	380
Ser Lys Asn Glu Val Glu Asp Ile Met Lys Arg Ile Lys Thr Asn Gly		
385	390	395
Arg Ser Asn Glu Asp Ile Ala Asn Gln Ile Ala Lys Gln Ile Asp Gly		
405	410	415
Leu Ala Leu Thr Ser Ser Asp Asp Ile Leu Lys Ser Met Leu Asp Gln		
420	425	430
Ser Lys Asp Lys Glu Ser Leu Ile Lys Gln Leu Leu Thr Thr Arg Leu		
435	440	445
Gly Asn Asp Glu Ala Asp Arg Ile Ala Lys Lys Leu Leu Ser Gln Asn		
450	455	460
Leu Ser Asn Ser Gln Ile Val Glu Gln Leu Lys Arg His Phe Asn Ser		
465	470	475
Gln Gly Thr Ala Thr Ala Asp Asp Ile Leu Asn Gly Val Ile Asn Asp		
485	490	495
Ala Lys Asp Lys Arg Gln Ala Ile Glu Thr Ile Leu Gln Thr Arg Ile		
500	505	510
Asn Lys Asp Lys Ala Lys Ile Ile Ala Asp Val Ile Ala Arg Val Gln		
515	520	525
Lys Asp Lys Ser Asp Ile Met Asp Leu Ile His Ser Ala Ile Glu Gly		
530	535	540
Lys Ala Asn Asp Leu Leu Asp Ile Glu Lys Arg Ala Lys Gln Ala Lys		
545	550	555
Lys Asp Leu Glu Tyr Ile Leu Asp Pro Ile Lys Asn Arg Pro Ser Leu		
565	570	575
Leu Asp Arg Ile Asn Lys Gly Val Gly Asp Ser Asn Ser Ile Phe Asp		
580	585	590

Arg Pro Ser Leu Leu Asp Lys Leu His Ser Arg Gly Ser Ile Leu Asp
595 600 605

Lys Leu Asp His Ser Ala Pro Glu Asn Gly Leu Ser Leu Asp Asn Lys
610 615 620

Gly Gly Leu Leu Ser Asp Leu Phe Asp Asp Asp Gly Asn Ile Ser Leu
625 630 635 640

Pro Ala Thr Gly Glu Val Ile Lys Gln His Trp Ile Pro Val Ala Val
645 650 655

Val Leu Met Ser Leu Gly Gly Ala Leu Ile Phe Met Ala Arg Arg Lys
660 665 670

Lys His Gln Asn
675

<210> 33
<211> 655
<212> PRT
<213> Staphylococcus epidermidis

<400> 33

Met Lys Lys Asn Lys Phe Leu Val Tyr Leu Leu Ser Thr Ala Leu Ile
1 5 10 15

Thr Pro Thr Phe Ala Thr Gln Thr Ala Phe Ala Glu Asp Ser Ser Asn
20 25 30

Lys Asn Thr Asn Ser Asp Lys Met Glu Gln His Gln Ser Gln Lys Glu
35 40 45

Thr Ser Lys Gln Ser Glu Lys Asp Glu Phe Asn Asn Asp Asp Ser Lys
50 55 60

His Asp Ser Asp Asp Lys Lys Ser Thr Ser Asp Ser Lys Asp Lys Asp
65 70 75 80

Ser Asn Lys Pro Leu Ser Ala Asp Ser Thr His Arg Asn Tyr Lys Met
85 90 95

Lys Asp Asp Asn Leu Val Asp Gln Leu Tyr Asp Asn Phe Lys Ser Gln
100 105 110

Ser Val Asp Phe Ser Lys Tyr Trp Glu Pro Asn Lys Tyr Glu Asp Ser
115 120 125

Phe Ser Leu Thr Ser Leu Ile Gln Asn Leu Phe Asp Phe Asp Ser Asp
130 135 140

Ile Thr Asp Tyr Glu Gln Pro Gln Lys Thr Ser His Ser Ser Asn Asp
145 150 155 160

Glu Lys Asp Gln Val Asp Gln Ala Asp Gln Ala Lys Gln Pro Ser Gln
165 170 175

His Gln Glu Pro Ser Gln Ser Ser Ala Lys Gln Asp Gln Glu Pro Ser
180 185 190

Asn Asp Glu Lys Glu Lys Thr Thr Asn His Gln Ala Asp Ser Asp Val
195 200 205

Ser Asp Leu Leu Gly Glu Met Asp Lys Glu Asp Gln Glu Gly Glu Asn
210 215 220

Val Asp Thr Asn Lys Asn Gln Ser Ser Ser Glu Gln Gln Gln Thr Gln
225 230 235 240

Ala Asn Asp Asp Ser Ser Glu Arg Asn Lys Lys Tyr Ser Ser Ile Thr
245 250 255

Asp Ser Ala Leu Asp Ser Ile Leu Asp Glu Tyr Ser Gln Asp Ala Lys
260 265 270

Lys Thr Glu Lys Asp Tyr Asn Lys Ser Lys Asn Thr Ser His Thr Lys
275 280 285

Thr Ser Gln Ser Asp Asn Ala Asp Lys Asn Pro Gln Leu Pro Thr Asp
290 295 300

Asp Glu Leu Lys His Gln Ser Lys Pro Ala Gln Ser Phe Glu Asp Asp
305 310 315 320

Ile Lys Arg Ser Asn Thr Arg Ser Thr Ser Leu Phe Gln Gln Leu Pro
325 330 335

Glu Leu Asp Asn Gly Asp Leu Ser Ser Asp Ser Phe Asn Val Val Asp
340 345 350

Ser Gln Asp Thr Arg Asp Phe Ile Gln Ser Ile Ala Lys Asp Ala His

355		360		365
Gln Ile Gly Lys Asp Gln Asp Ile Tyr Ala Ser Val Met Ile Ala Gln				
370		375		380
Ala Ile Leu Glu Ser Asp Ser Gly Lys Ser Ser Leu Ala Gln Ser Pro				
385		390		395 400
Asn His Asn Leu Phe Gly Ile Lys Gly Asp Tyr Lys Gly Gln Ser Val				
	405		410	415
Thr Phe Asn Thr Leu Glu Ala Asp Ser Ser Asn His Met Phe Ser Ile				
	420		425	430
Gln Ala Gly Phe Arg Lys Tyr Pro Ser Thr Lys Gln Ser Leu Glu Asp				
	435		440	445
Tyr Ala Asp Leu Ile Lys His Gly Ile Asp Gly Asn Pro Ser Ile Tyr				
450		455		460
Lys Pro Thr Trp Lys Ser Glu Ala Leu Ser Tyr Lys Asp Ala Thr Ser				
465		470		475 480
His Leu Ser Arg Ser Tyr Ala Thr Asp Pro Asn Tyr Ser Lys Lys Leu				
	485		490	495
Asn Ser Ile Ile Lys His Tyr His Leu Thr Ser Phe Asp Lys Glu Lys				
	500		505	510
Met Pro Asn Met Lys Lys Tyr Asn Lys Ser Ile Gly Thr Asp Val Ser				
	515		520	525
Gly Asn Asp Phe Lys Pro Phe Thr Glu Thr Ser Gly Thr Ser Pro Tyr				
530		535		540
Pro His Gly Gln Cys Thr Trp Tyr Val Tyr His Arg Met Asn Gln Phe				
545		550		555 560
Asp Ala Ser Ile Ser Gly Asp Leu Gly Asp Ala His Asn Trp Asn Asn				
	565		570	575
Arg Ala Glu Ser Glu Gly Tyr Thr Val Thr His Thr Pro Lys Asn His				
	580		585	590
Thr Ala Val Val Phe Glu Ala Gly Gln Leu Gly Ala Asp Thr Gln Tyr				
595		600		605

Gly His Val Ala Phe Val Glu Lys Val Asn Asp Asp Gly Ser Ile Val
610 615 620

Ile Ser Glu Ser Asn Val Lys Gly Leu Gly Val Ile Ser Phe Arg Thr
625 630 635 640

Ile Asp Ala Gly Asp Ala Gln Asp Leu Asp Tyr Ile Lys Gly Lys
645 650 655

<210> 34
<211> 164
<212> PRT
<213> Staphylococcus epidermidis

<400> 34

Met Ile Arg Phe Ala Arg Leu Glu Asp Leu Gln Asp Ile Leu Thr Ile
1 5 10 15

Tyr Asn Asp Ala Ile Leu Asn Thr Thr Ala Val Tyr Thr Tyr Lys Pro
20 25 30

Gln Gln Leu Asp Glu Arg Leu Gln Trp Tyr Gln Ser Lys Ala Lys Ile
35 40 45

Asn Glu Pro Ile Trp Val Tyr Glu Lys Glu Gly Lys Val Val Gly Phe
50 55 60

Ala Thr Tyr Gly Ser Phe Arg Gln Trp Pro Ala Tyr Leu Tyr Thr Ile
65 70 75 80

Glu His Ser Ile Tyr Val His Gln Gln Tyr Arg Gly Leu Gly Ile Ala
85 90 95

Ser Gln Leu Leu Glu Asn Leu Ile Arg Tyr Ala Lys Glu Gln Gly Tyr
100 105 110

Arg Thr Ile Val Ala Gly Ile Asp Ala Ser Asn Met Asp Ser Ile Ala
115 120 125

Leu His Lys Lys Phe Asp Phe Ser His Ala Gly Thr Ile Lys Asn Val
130 135 140

Gly Tyr Lys Phe Asp Arg Trp Leu Asp Leu Ser Phe Tyr Gln Tyr Asp
145 150 155 160

Leu Ser Asp Ser

<210> 35
<211> 952
<212> PRT
<213> Staphylococcus epidermidis

<400> 35

Leu Ser Asn Leu Ile Gln Asp Ile Lys Gln Ser Leu Tyr Lys Gly Phe
1 5 10 15

Ile Asp Lys Asp Ser Ser His Lys Gly Asn Phe Val Pro Arg Leu Leu
20 25 30

Val Asn Asn Lys Glu Glu Asn Val Leu Ser Thr Ile Ile Asp Gln Leu
35 40 45

His Asn Cys Gln Ser Phe Cys Ile Ser Val Ala Phe Ile Thr Glu Ser
50 55 60

Gly Leu Ala Ser Leu Lys Ser His Phe Tyr Asp Leu Ser Lys Lys Gly
65 70 75 80

Val Lys Gly Arg Ile Ile Thr Ser Asn Tyr Leu Gly Phe Asn Ser Pro
85 90 95

Lys Met Phe Glu Glu Leu Leu Lys Leu Glu Asn Val Glu Val Lys Leu
100 105 110

Thr Asn Ile Glu Gly Phe His Ala Lys Gly Tyr Ile Phe Glu His His
115 120 125

Asn His Thr Ser Phe Ile Ile Gly Ser Ser Asn Leu Thr Ser Asn Ala
130 135 140

Leu Lys Leu Asn Tyr Glu His Asn Leu Phe Leu Ser Thr His Lys Asn
145 150 155 160

Gly Asp Leu Val Asn Asn Ile Lys Tyr Lys Phe Asp Glu Leu Trp Asp
165 170 175

Ser Ser Phe Ser Leu Thr Asn Glu Trp Ile Asn Glu Tyr Lys Gln Ser
180 185 190

Phe Glu Tyr Gln Thr Leu Gln Lys Val Phe Asp Asn Thr Val Val Gln
195 200 205

Asn Ser Asp Ile Lys Lys Phe Asn Glu Ser Lys Leu Ile Lys Pro Asn
210 215 220

Leu Met Gln Glu His Ala Leu Lys Ser Leu Glu Ser Leu Arg Asn Val
225 230 235 240

Gly Glu Glu Lys Gly Leu Ile Ile Ser Ala Thr Gly Thr Gly Lys Thr
245 250 255

Ile Leu Cys Ala Leu Asp Val Arg Ala Tyr Ser Pro Asp Lys Phe Leu
260 265 270

Phe Ile Val His Asn Glu Gly Ile Leu Asn Arg Ala Ile Glu Glu Phe
275 280 285

Lys Lys Val Phe Pro Tyr Glu Asp Glu Ser Asn Phe Gly Leu Leu Thr
290 295 300

Gly Lys Arg Lys Asp His Asp Ala Lys Phe Leu Phe Ala Thr Ile Gln
305 310 315 320

Thr Leu Ser Lys Lys Glu Asn Tyr Lys Leu Phe Asn Ser Asn His Phe
325 330 335

Asp Tyr Ile Val Phe Asp Glu Ala His Arg Ile Ala Ala Ser Ser Tyr
340 345 350

Gln Lys Ile Phe Asn Tyr Phe Lys Pro Asn Phe Leu Leu Gly Met Thr
355 360 365

Ala Thr Pro Glu Arg Thr Asp Glu Leu Asn Ile Phe Glu Leu Phe Asn
370 375 380

Tyr Asn Ile Ala Tyr Glu Ile Arg Leu Gln Glu Ala Leu Glu Ser Asn
385 390 395 400

Ile Leu Cys Pro Phe His Tyr Phe Gly Val Thr Asp Tyr Ile Gln Asn
405 410 415

Glu Met Ser Gln Glu Asp Ala Phe Asn Leu Lys Tyr Leu Ala Ser Asn
420 425 430

Glu Arg Val Glu His Ile Ile Lys Lys Thr Asn Tyr Tyr Gly Tyr Ser
435 440 445

Gly Asp Val Leu Lys Gly Leu Ile Phe Val Ser Ser Arg Gly Glu Ala
450 455 460

Tyr Gln Leu Ala Asn Gln Leu Ser Lys Arg Gly Ile Ser Ser Val Gly
465 470 475 480

Leu Thr Gly Lys Asp Ser Ile Ala Tyr Arg Ala Glu Thr Ile Gln Gln
485 490 495

Leu Lys Glu Gly Ser Ile Asn Tyr Ile Ile Thr Val Asp Leu Phe Asn
500 505 510

Glu Gly Ile Asp Ile Pro Glu Ile Asn Gln Val Val Met Leu Arg Pro
515 520 525

Thr Lys Ser Ser Ile Ile Phe Ile Gln Gln Leu Gly Arg Gly Leu Arg
530 535 540

Lys Ser Thr Asn Lys Glu Phe Val Thr Val Ile Asp Phe Ile Gly Asn
545 550 555 560

Tyr Lys Thr Asn Tyr Met Ile Pro Ile Ala Leu Ser Gly Asn Lys Ser
565 570 575

Gln Asn Lys Asp Asn Tyr Arg Lys Phe Leu Thr Asp Thr Thr Val Leu
580 585 590

Asn Gly Val Ser Thr Ile Asn Phe Glu Glu Val Ala Lys Asn Lys Ile
595 600 605

Tyr Asn Ser Leu Asp Ser Val Lys Leu Asn Gln Pro Lys Leu Ile Lys
610 615 620

Glu Ala Phe Asn Asn Val Lys Asp Arg Ile Gly Lys Leu Pro Leu Leu
625 630 635 640

Met Asp Phe Ile Asn Asn Asp Ser Ile Asp Pro Ser Val Ile Phe Ser
645 650 655

Arg Phe Lys Asn Tyr Tyr Glu Phe Leu Ile Lys Asn Lys Ile Ile Glu
660 665 670

Asn Glu Leu Ser Ile Asn Glu Phe Lys Asn Leu Thr Phe Leu Ser Arg
675 680 685

Gln Leu Thr Pro Gly Leu Lys Lys Val Asp Ile Asp Val Leu Lys Glu
690 695 700

Ile Ile Gln Asn Asp Val Thr Tyr Glu Asn Leu Thr Lys Lys Met Leu
705 710 715 720

Asn Ile Asn Asn Asp Ile Ser Glu Tyr Asp Ile Asn Thr Ser Leu Ser
725 730 735

Ile Leu Asp Phe Thr Phe Phe Lys Lys Thr Ile Gly Lys Thr Tyr Gly
740 745 750

Leu Pro Leu Ile Gln Tyr Lys Asp Asn Leu Ile Cys Leu Ala Asn Glu
755 760 765

Phe Lys Glu Ala Leu Asn Lys Pro Leu Phe Asn Thr Phe Ile His Asp
770 775 780

Leu Ile Asp Leu Ala Asn Tyr Asn Asn Asp Arg Tyr Gln Asn Lys Lys
785 790 795 800

Asn Ser Leu Ile Leu Tyr Asn Lys Tyr Ser Arg Glu Asp Phe Val Lys
805 810 815

Leu Leu Asn Trp Asp Lys Asp Glu Ser Gly Thr Ile Asn Gly Tyr Arg
820 825 830

Met Lys His Arg Thr Leu Pro Leu Phe Ile Thr Tyr Asp Lys His Glu
835 840 845

Asn Ile Ser Asp Asn Thr Lys Tyr Asp Asp Glu Phe Leu Ser Gln Asp
850 855 860

Glu Leu Lys Trp Tyr Thr Arg Ser Asn Arg Lys Leu Thr Ser Pro Glu
865 870 875 880

Val Gln Asn Ile Leu Lys His Glu Glu Ser Asn Thr Asp Met Tyr Ile
885 890 895

Phe Val Lys Lys Arg Asp Asp Glu Gly Lys Tyr Phe Tyr Tyr Leu Gly
900 905 910

Lys Ala Lys Tyr Ile Lys Gly Thr Glu Lys Gln Asp Tyr Met Pro Asn
915 920 925

Gly Asn Ser Val Val Thr Met His Leu Ser Met Asn Thr Ser Ile Arg

930

935

940

Asp Asp Ile Tyr Arg Tyr Ile Thr
945 950

<210> 36
<211> 325
<212> PRT
<213> Staphylococcus epidermidis

<400> 36

Met Thr Lys Ser Gln Gln Lys Val Ser Ser Ile Glu Lys Leu Ser Asn
1 5 10 15

Gln Glu Gly Ile Ile Ser Ala Leu Ala Phe Asp Gln Arg Gly Ala Leu
20 25 30

Lys Arg Met Met Ala Glu His Gln Ser Glu Thr Pro Thr Val Glu Gln
35 40 45

Ile Glu Gln Leu Lys Val Leu Val Ser Glu Glu Leu Thr Gln Tyr Ala
50 55 60

Ser Ser Ile Leu Leu Asp Pro Glu Tyr Gly Leu Pro Ala Ser Asp Ala
65 70 75 80

Arg Asn Asn Asp Cys Gly Leu Leu Leu Ala Tyr Glu Lys Thr Gly Tyr
85 90 95

Asp Val Asn Ala Lys Gly Arg Leu Pro Asp Cys Leu Val Glu Trp Ser
100 105 110

Ala Lys Arg Leu Lys Glu Gln Gly Ala Asn Ala Val Lys Phe Leu Leu
115 120 125

Tyr Tyr Asp Val Asp Asp Thr Glu Glu Ile Asn Ile Gln Lys Lys Ala
130 135 140

Tyr Ile Glu Arg Ile Gly Ser Glu Cys Val Ala Glu Asp Ile Pro Phe
145 150 155 160

Phe Leu Glu Val Leu Thr Tyr Asp Asp Asn Ile Pro Asp Asn Lys Ser
165 170 175

Ala Glu Phe Ala Lys Val Lys Pro Arg Lys Val Asn Glu Ala Met Lys
180 185 190

Leu Phe Ser Glu Asp Arg Phe Asn Val Asp Val Leu Lys Val Glu Val
195 200 205

Pro Val Asn Met Asn Phe Val Glu Gly Phe Ser Glu Gly Glu Val Val
210 215 220

Tyr Thr Lys Glu Glu Ala Ala Gln His Phe Arg Asp Gln Asp Ala Ala
225 230 235 240

Thr His Leu Pro Tyr Ile Tyr Leu Ser Ala Gly Val Ser Ala Glu Leu
245 250 255

Phe Gln Asp Thr Leu Lys Phe Ala His Asp Ser Gly Ala Gln Phe Asn
260 265 270

Gly Val Leu Cys Gly Arg Ala Thr Trp Ser Gly Ala Val Lys Val Tyr
275 280 285

Ile Glu Glu Gly Glu Gln Ala Ala Arg Glu Trp Leu Arg Thr Val Gly
290 295 300

Phe Lys Asn Ile Asp Asp Leu Asn Thr Val Leu Lys Thr Thr Ala Thr
305 310 315 320

Ser Trp Lys Asn Lys
325

<210> 37
<211> 382
<212> PRT
<213> Staphylococcus epidermidis

<400> 37

Leu Met Lys Lys Val Met Thr Ile Phe Gly Thr Arg Pro Glu Ala Ile
1 5 10 15

Lys Met Ala Pro Leu Ile Lys Thr Leu Glu Lys Asp Ser Asp Leu Glu
20 25 30

Pro Val Val Val Val Thr Ala Gln His Arg Glu Met Leu Asp Ser Val
35 40 45

Leu Asn Thr Phe Asn Ile Ser Ala Asp Tyr Asp Leu Asn Ile Met Lys
50 55 60

Ala Gly Gln Thr Leu Ser Glu Val Thr Ser Glu Ala Met Lys Lys Leu

65		70		75		80
Glu Asp Ile Ile Gln Lys Glu Val Pro Asp Met Val Leu Val His Gly	85	90	95			
Asp Thr Val Thr Thr Phe Ser Gly Ala Leu Ala Ala Phe Tyr Ser Gln	100	105	110			
Thr Pro Ile Gly His Val Glu Ala Gly Leu Arg Ser Tyr Asn Lys Tyr	115	120	125			
Ser Pro Tyr Pro Glu Glu Ile Asn Arg Gln Met Val Gly Val Met Ala	130	135	140			
Asp Leu His Phe Ala Pro Thr Tyr Asn Ala Ala Gln Asn Leu Val Lys	145	150	155			160
Glu Gly Lys Leu Ala Lys His Ile Ala Ile Thr Gly Asn Thr Ala Ile	165	170	175			
Asp Ala Met Asn Tyr Thr Ile Asp His Gln Tyr Ser Ser Ser Ile Ile	180	185	190			
Gln Lys His Lys Asn Lys Asn Phe Ile Leu Leu Thr Ala His Arg Arg	195	200	205			
Glu Asn Ile Gly Lys Pro Met Ile Asn Val Phe Lys Ala Ile Arg Lys	210	215	220			
Leu Ile Asp Glu Tyr Gln Asp Leu Ala Leu Val Tyr Pro Met His Met	225	230	235			240
Asn Pro Lys Val Arg Asp Ile Ala Gln Lys Tyr Leu Gly Asn His Pro	245	250	255			
Arg Ile Glu Leu Ile Glu Pro Leu Asp Val Val Asp Phe His Asn Phe	260	265	270			
Ala Lys Gln Ala Tyr Leu Ile Met Thr Asp Ser Gly Gly Ile Gln Glu	275	280	285			
Glu Ala Pro Ser Leu His Lys Pro Val Leu Val Leu Arg Asp Ser Thr	290	295	300			
Glu Arg Pro Glu Gly Val Asp Ala Gly Thr Leu Arg Val Ile Gly Thr	305	310	315			320

Asn Glu Glu Asp Val Tyr Asn Glu Thr Lys Lys Leu Ile Glu Asn Pro
325 330 335

Asp Leu Tyr Gln Lys Met Ser Gln Ala Val Asn Pro Tyr Gly Asp Gly
340 345 350

Gln Ala Ser Glu Arg Ile Val Gln His Ile Lys Tyr Tyr Phe Asn Leu
355 360 365

Thr Asn Asp Arg Pro Asn His Phe Glu Phe Thr Lys Asp Leu
370 375 380

<210> 38

<211> 2757

<212> PRT

<213> Staphylococcus epidermidis

<400> 38

Val Ala Ser Asp Phe Asn Ile Gly Ile Leu Ser Thr Leu Glu Ile Asp
1 5 10 15

Ser Ser Ser Ser Arg Lys Lys Ile Asn Asp Thr Leu Lys Asn Ile Glu
20 25 30

Ala Asn Ile Asn Ser Ile Lys Ala Asp Leu Glu Val Ser Asp Thr Lys
35 40 45

Lys Ser Glu Asn Asn Ala Ile Lys Ser Ala Asn Asn Val Ile Arg Asn
50 55 60

Ile Asn Ser Asn Gly Asn Leu Lys Lys Leu Asn Val Glu Leu Asp Val
65 70 75 80

Asn Leu Thr Lys Ser Arg Gln Asn Ile Gln Arg Ala Leu Ser Thr Leu
85 90 95

Ser Lys Asp Phe Lys Asn Lys Lys Ile Asp Val Glu Val Asn Ala Lys
100 105 110

Ala Asn Lys Asn Ser Ile Gly Gln Val Lys Asn Ser Ile Ser Lys Gly
115 120 125

Ala Ser Gln Pro Leu Glu Ile Lys Glu Ser Pro Ser Ser Arg Ser Thr
130 135 140

Ser Arg Asp Ile Lys Glu Gln Gln Ser Leu Met Thr Gly Leu Ala Asn
145 150 155 160

Ser Tyr Lys Asn Leu Asp Asp Leu Thr Arg Ala Leu Asn Thr Ser Thr
165 170 175

Phe Glu Gly Leu Arg Lys Thr Val Lys Glu Ile Lys Asn Ala Asp Asn
180 185 190

Ser Leu Lys Ser Tyr Gln Val Thr Leu Glu Arg Val Asn Gln Glu Gly
195 200 205

Lys Lys Leu Gly Ser Gln Arg Phe Asp Tyr Thr Pro Ser Ala Asn Gly
210 215 220

Leu Lys Leu Asn Lys Thr Gln Leu Thr Asp Gln Thr Asp Lys Ala Arg
225 230 235 240

Lys Glu Glu Asn Ala Ala Ile Asn Lys Leu Leu Glu Asn Glu Val Ser
245 250 255

Lys Tyr Asp Arg Leu Leu Asn Lys Gly Lys Ile Asp Ile Lys Gln His
260 265 270

Gln Thr Leu Leu Gln Thr Leu Arg Gln Ile Thr Asn Glu Lys Ser Lys
275 280 285

Ala Asn Gln Phe Asn Arg Thr Asp Phe Asn Arg Val Ala Lys Ala Ala
290 295 300

Ala Asp Glu Ala Lys Glu Tyr Gln Tyr Gln Asn Asp Met Leu Arg Lys
305 310 315 320

Lys Leu Ala Leu Thr Ser Gln Ile Glu Arg Ile Glu Asn Arg Met Ala
325 330 335

Ala Thr Ile Asp Lys Gln Gln Thr Asn Ala Leu Lys Asn Gln Leu Asn
340 345 350

Ser Leu Gly Asn Asn Arg Thr Pro Phe Gly Lys Glu Ala Ala Phe His
355 360 365

Met Asn Gln Ile Gln Asp Lys Val Arg Gln Ile Ser Ala Glu Ala Glu
370 375 380

Arg Ala Thr Arg Thr Gln Leu Ser Phe Val Asp Gln Phe Arg Glu Ala

385		390		395		400
Met Thr Lys Phe Pro Val Trp Met Gly Ala Thr Thr Leu Phe Phe Gly						
		405		410		415
Ala Ile Asn Gly Ala Lys Glu Met Leu Asp Val Ile Thr Glu Ile Asp						
		420		425		430
Gly Lys Met Ile Thr Leu Ala Lys Val Thr Gly Asp Asp Asn Ala Leu						
		435		440		445
Gln Gln Thr Phe Ile Asp Ala Asn Asn Ala Ala Ser Gln Phe Gly Gln						
		450		455		460
Thr Leu Gly Ser Val Leu Asp Val Tyr Ala Glu Phe Ala Arg Gln Gly						
		465		470		475
Val Lys Gly Asn Glu Leu Ser Gln Phe Ser Asn Ala Ala Leu Ile Ala						
		485		490		495
Ala Asn Val Gly Glu Ile Asp Ala Lys Gln Ala Ser Glu Tyr Leu Thr						
		500		505		510
Ser Met Ser Ala Gln Trp Glu Thr Thr Gly Asn Gln Ala Met Arg Gln						
		515		520		525
Val Asp Ser Leu Asn Glu Val Ser Asn Lys Tyr Ala Thr Thr Val Glu						
		530		535		540
Lys Leu Ala Gln Gly Gln Ala Lys Ala Gly Ser Thr Ala Lys Ser Met						
		545		550		555
Gly Leu Thr Phe Asp Glu Thr Asn Gly Ile Ile Gly Ala Leu Thr Ala						
		565		570		575
Lys Thr Lys Gln Ser Gly Asp Glu Ile Gly Asn Phe Met Lys Ala Thr						
		580		585		590
Leu Pro Lys Leu Tyr Ser Gly Lys Gly Lys Ser Thr Ile Glu Gly Leu						
		595		600		605
Gly Ile Ser Met Lys Asp Glu Asn Gly Gln Leu Lys Ser Ala Ile Ser						
		610		615		620
Leu Leu Glu Glu Val Ser Gln Lys Thr Lys Asn Leu Glu Lys Asp Gln						
		625		630		635
						640

Lys Ala Ala Val Ile Asn Gly Leu Gly Gly Thr Tyr His Tyr Gln Arg
645 650 655

Met Gln Val Leu Leu Asp Asp Leu Ser Lys Thr Asp Gly Leu Tyr Lys
660 665 670

Gln Ile Lys Glu Ser Ser Glu Ser Ser Ala Gly Ser Ala Leu Gln Glu
675 680 685

Asn Ala Lys Tyr Met Glu Ser Ile Glu Ala Lys Val Asn Gln Ala Lys
690 695 700

Thr Ala Phe Glu Gln Phe Ala Leu Ala Val Gly Glu Thr Phe Ala Lys
705 710 715 720

Ser Gly Met Leu Asp Gly Ile Arg Met Val Thr Gln Leu Leu Thr Gly
725 730 735

Leu Thr His Gly Ile Thr Glu Leu Gly Thr Thr Ala Pro Ile Phe Gly
740 745 750

Met Val Gly Gly Ala Ala Ser Leu Met Ser Lys Asn Val Arg Ser Gly
755 760 765

Phe Glu Gly Ala Arg Ser Ser Val Ala Asn Tyr Ile Thr Glu Val Asn
770 775 780

Lys Leu Ala Lys Val Asn Asn Ala Ala Gly Gln Val Val Gly Leu Gln
785 790 795 800

Lys Val Gln Thr Gly Thr Ala Ser Gln Leu Gln Phe Asn Lys Asn Gly
805 810 815

Glu Tyr Asp Lys Ala Ala Ser Gln Ala Lys Ala Ala Glu Gln Ala Thr
820 825 830

Tyr Gln Phe Ser Lys Ala Gln Lys Asp Val Ser Ala Ser Ala Met Ile
835 840 845

Ala Ser Gly Ala Ile Asn Lys Thr Thr Val Ala Thr Thr Ala Ser Thr
850 855 860

Val Ala Thr Arg Ala Ala Thr Leu Ala Val Asn Gly Leu Lys Leu Ala
865 870 875 880

Phe Arg Gly Leu Leu Ala Ala Thr Gly Val Gly Leu Ala Ile Thr Gly
885 890 895

Val Ser Phe Val Leu Glu Lys Val Val Gly Ser Phe Asn Ala Ala Ser
900 905 910

Gln Ala Ala Glu Gln Tyr Lys Gln Lys Gln Glu Gln Thr Lys Gln Ala
915 920 925

Ile Ala Ser Met Ser Asn Gly Glu Ile Asn Ser Leu Ile Ser Ser Tyr
930 935 940

Asp Lys Leu Gln Gln Lys Met Asn Ser Gly Ser Ala Phe Asn Thr Ala
945 950 955 960

Glu Ala Glu Lys Tyr Lys Glu Val Thr Ser Gln Leu Ala Asn Ile Phe
965 970 975

Pro Asp Leu Val Thr Gly Glu Asn Arg Tyr Gly Lys Glu Met Ala Gly
980 985 990

Asn Lys Glu Val Met Lys Gln Lys Ile Glu Leu Ile Lys Gln Glu Met
995 1000 1005

Glu Leu Glu Arg Gln Lys Asn Ala Ile Lys Gln Lys Glu Glu Gln
1010 1015 1020

Asp Ala Tyr Ile Lys Glu Gln Asp Ser Leu Ala Lys Lys Asn Arg
1025 1030 1035

Gly Gln Lys Trp Tyr Gln Leu Gly Gln Thr Pro Glu Leu Lys Leu
1040 1045 1050

Gln Glu Gln Ala Arg Pro Thr Thr Val Ser Asp Asn Ser Asn Ile
1055 1060 1065

Asn Lys Ile Asn Ala Thr Ile Gln Lys Val Lys Ser Gln Ala Gln
1070 1075 1080

Ala Glu Lys Ala Leu Glu Gln Val Asp Lys Gln Leu Ala Gln Ser
1085 1090 1095

Gln Thr Lys Asn Arg Gln Asn Glu Val Gln His Leu Gln Lys Val
1100 1105 1110

Arg	Gln	Ala	Leu	Gln	Asp	Tyr	Ile	Thr	Lys	Thr	Gly	Gln	Ala	Asn
1115						1120					1125			
Gln	Ala	Thr	Arg	Ala	Ala	Val	Leu	Thr	Ala	Gln	Gln	Gln	Phe	Thr
1130						1135					1140			
Asn	Gln	Ile	Ala	Thr	Met	Lys	Lys	Leu	Gly	Thr	Thr	Gly	Gln	Gln
1145						1150					1155			
Val	Met	Thr	Thr	Ile	Ser	Asn	Ser	Val	Ala	Lys	Thr	Ala	Lys	Ser
1160						1165					1170			
Gly	Lys	Ala	Ala	Gln	Ala	Thr	Phe	Lys	Ser	Phe	Glu	Thr	Ser	Leu
1175						1180					1185			
Val	Lys	Ser	Ser	Ser	Phe	Lys	Ser	Lys	Met	Ala	Ser	Tyr	Glu	Ala
1190						1195					1200			
Ser	Val	Lys	Lys	Phe	Lys	Asn	Ala	Ala	Asn	Gln	Ser	Ala	Lys	Ile
1205						1210					1215			
Ala	Ala	Leu	Lys	Asp	Val	Glu	Arg	Asp	Tyr	Ser	Lys	Val	Ala	Lys
1220						1225					1230			
Gly	Ile	Met	Gln	Ala	Ala	Lys	Ala	Ala	Asn	Met	Ser	Lys	Ser	Gln
1235						1240					1245			
Met	Lys	Asp	Leu	Lys	Lys	Ser	Leu	Gln	Gln	Asn	Ile	Gln	Ala	Glu
1250						1255					1260			
Thr	Gly	Phe	Arg	Ala	Ser	Val	Ser	Lys	Ala	Gly	Lys	Val	Thr	Ile
1265						1270					1275			
Asp	Gln	Ser	Lys	Lys	Ile	Lys	Gln	Asn	Thr	Ala	Glu	Thr	Arg	Arg
1280						1285					1290			
Asn	Ser	Ser	Ala	Lys	Leu	Gln	Asn	Ala	Asp	Ala	Ser	Asp	Gln	Ala
1295						1300					1305			
Ser	Glu	Glu	Asn	Lys	Glu	Leu	Ala	Asp	Ser	Met	Arg	Ala	Gly	Ile
1310						1315					1320			
Glu	Ser	Ser	Gln	Leu	Leu	Gly	Lys	Ala	Met	Gly	Glu	Leu	Gln	Ser
1325						1330					1335			
Gln	Gly	Thr	Leu	Ser	Thr	Glu	Thr	Leu	Ile	Glu	Leu	Thr	Glu	Lys

1340		1345		1350
Tyr Gly Asp Glu Ile Leu Ala Val Ala Gly Asp Gln Glu Ala Leu				
1355		1360		1365
Ser Asn Phe Ile Met Gln Lys Gln Asn Glu Glu Thr Asp Asn Tyr				
1370		1375		1380
Asn Lys Asn Leu Lys Thr Lys Leu Glu Asn Ser Ser Ser Tyr Tyr				
1385		1390		1395
Lys Ala Val Ala Gly Ala Asp Ser Ala Leu Ser Asn Tyr Leu Met				
1400		1405		1410
Glu Asn Tyr Gly Ile Asp Thr Lys Asn Tyr Lys Ser Leu Thr Glu				
1415		1420		1425
Val Lys Ala Lys Ile Thr Asp Leu Tyr Tyr Asn Gly Ser Ala Glu				
1430		1435		1440
Glu Gln Ala Lys Val Val Asp Ala Ile Ala Lys Ala Tyr His Ile				
1445		1450		1455
Asp Leu Ser Asn Tyr Gly Ser Leu Asn Glu Lys Lys Glu Ala Leu				
1460		1465		1470
Glu Asn Gln Leu Met Lys Ile Leu Gly Ser Lys Trp Lys Lys Tyr				
1475		1480		1485
Ile Gly Ser Val Ala Lys Asp Met Lys Ser Leu Gly Val Asp Ala				
1490		1495		1500
Gly Glu Val Gly Ala Asp Gly Phe Asp Asp Ser Lys Met Phe Asn				
1505		1510		1515
Pro Gly Ala Leu Ile Gly Ala Asn Asn Phe Gln Asn Val Ser Asn				
1520		1525		1530
Leu Ser Asn Ile Ser Asn Val Phe Asn Ser Leu Asn Gly Ala Phe				
1535		1540		1545
Asn Glu Ala Lys Asn Glu Ala Ala Gly Val Ser Arg Gly Leu Asp				
1550		1555		1560
Asp Ala Ala Ser Gly Leu Lys Asp Val Gly Asp Ser Ala Gly Ser				
1565		1570		1575

Ala Gly	Ser Gly	Leu Gly	Lys	Thr Ala	Lys Gly	Ala	Asp Lys	Ala	
1580			1585			1590			
Ser Asp	Ser Leu	Asp Gly	Thr	Asn Lys	Glu Leu	Glu	Lys Thr	Lys	
1595			1600			1605			
Glu Lys	Ala Glu	Glu Ala	Gly	Val Thr	Val Lys	Gln	Leu Tyr	Lys	
1610			1615			1620			
Gln Phe	Thr Val	Thr Thr	Tyr	Val Ala	Asp Lys	Leu	Ser Met	Ala	
1625			1630			1635			
Leu Asp	Lys Ile	Asn Asn	Lys	Leu Glu	Lys Gln	Lys	Leu Leu	Thr	
1640			1645			1650			
Glu Lys	Tyr Ala	Thr Trp	Ser	Ser Ser	Tyr Arg	Asn	Ser Leu	Lys	
1655			1660			1665			
Ala Glu	Asn Lys	Leu Leu	Asp	Glu Lys	Thr Ala	Lys	Ile Lys	Lys	
1670			1675			1680			
Gln Ile	Glu Ser	Met Lys	Glu	Gln Ile	Ala Gln	Gly	Lys Val	Ile	
1685			1690			1695			
Glu Tyr	Gly Leu	Val Gly	Lys	Asp Ile	Asn Val	Pro	Tyr Tyr	Glu	
1700			1705			1710			
Tyr Thr	Ala Asn	Asn Leu	Asp	Asp Gly	Glu Thr	Gly	Arg Ile	Ser	
1715			1720			1725			
Arg Tyr	Thr Gly	Asn Ser	Thr	Gln Ala	Lys Val	Trp	Asn Phe	Phe	
1730			1735			1740			
Lys Ser	Lys Gly	Leu Ser	Asp	His Ala	Val Ala	Gly	Ile Met	Gly	
1745			1750			1755			
Asn Met	Glu Arg	Glu Ser	Arg	Phe Lys	Pro Gly	Ala	Gln Glu	Gln	
1760			1765			1770			
Gly Gly	Thr Gly	Ile Gly	Leu	Val Gln	Leu Ser	Phe	Gly Arg	Ala	
1775			1780			1785			
Asn Asn	Leu Arg	Asn Tyr	Ala	Ala Arg	Arg Gly	Lys	Ser Trp	Lys	
1790			1795			1800			

Asp	Leu	Asn	Thr	Gln	Leu	Asp	Phe	Ile	Trp	Lys	Glu	Leu	Asn	Thr
1805						1810					1815			
Thr	Glu	Val	Asn	Ala	Leu	Arg	Gly	Leu	Lys	Ser	Ala	Thr	Ser	Val
1820						1825					1830			
Ile	Gly	Ala	Ala	Asn	Ser	Phe	Gln	Arg	Leu	Tyr	Glu	Arg	Ala	Gly
1835						1840					1845			
Val	Val	Ala	Gln	Gly	Glu	Arg	Asn	Ala	Ala	Ala	Lys	Lys	Tyr	Tyr
1850						1855					1860			
Arg	Gln	Phe	Lys	Gly	Thr	Asn	Gly	Ser	Ser	Gly	Phe	Leu	Ser	Gly
1865						1870					1875			
Gly	Val	Val	Ala	Gly	Thr	Asn	Gly	Lys	Pro	Leu	Thr	Ser	Asp	Arg
1880						1885					1890			
Asn	Ala	Tyr	Ile	Leu	Asp	Arg	Gln	Phe	Gly	Arg	Tyr	Asn	Gly	Gly
1895						1900					1905			
Gly	Val	His	His	Gly	Arg	Asp	Ile	Thr	Ser	Ala	Thr	Ile	Asn	Gly
1910						1915					1920			
Ser	Pro	Ile	Lys	Ala	Ala	Arg	Ser	Gly	Ile	Val	Thr	Phe	Lys	Gly
1925						1930					1935			
Trp	Thr	Gly	Gly	Gly	Asn	Thr	Leu	Ser	Ile	Phe	Asp	Gly	Lys	Asn
1940						1945					1950			
Thr	Tyr	Thr	Tyr	Met	His	Met	Lys	Asn	Pro	Ala	Arg	Val	Val	Lys
1955						1960					1965			
Gly	Gln	Arg	Val	Lys	Ala	Gly	Gln	Ile	Val	Gly	Asn	Val	Gly	Thr
1970						1975					1980			
Thr	His	Asp	Arg	Arg	Leu	Gly	Gly	Phe	Ser	Thr	Gly	Pro	His	Leu
1985						1990					1995			
His	Val	Gln	Val	Asn	Leu	Gly	Lys	Thr	Pro	Ser	Gly	Thr	Phe	Met
2000						2005					2010			
Asn	Thr	Phe	Asn	Gly	Ala	His	Arg	Ala	Val	Asp	Pro	Val	Lys	Tyr
2015						2020					2025			

Gly	Tyr	Thr	Arg	Val	Ser	Gly	Gly	Gly	Ser	Leu	Asn	Leu	Gly	Ser
2030						2035					2040			
Leu	Thr	Ser	Gly	His	Ser	Ala	Met	Ser	Gly	Ser	Ile	Ser	Ala	Ala
2045						2050					2055			
Met	Ala	Glu	Asp	Leu	Asn	Glu	Ala	Glu	Gln	Glu	Arg	Leu	Asn	Lys
2060						2065					2070			
Ile	Glu	Gln	Ala	Ile	Asn	Ala	His	Asn	Lys	Ala	Glu	Glu	Met	Lys
2075						2080					2085			
Gln	Lys	Val	Asp	Glu	Leu	Arg	Lys	Thr	Leu	Met	Asp	Lys	Gln	Leu
2090						2095					2100			
Glu	Glu	Val	Gln	Thr	Ala	Lys	Glu	Lys	Ser	Glu	Asn	Leu	Tyr	Asn
2105						2110					2115			
Ile	Gln	Lys	Ser	His	Val	Glu	Glu	Tyr	Asp	His	Trp	Arg	Thr	Leu
2120						2125					2130			
Gln	Glu	Ala	Arg	Ser	Ala	Lys	Leu	Glu	Tyr	Glu	Leu	Asn	Lys	Ile
2135						2140					2145			
Glu	Phe	Glu	Lys	Gly	Arg	Asn	Thr	Lys	Glu	Trp	Arg	Asn	Lys	Asn
2150						2155					2160			
Lys	Gln	Leu	Gln	Ala	Ser	Arg	Gln	Leu	Glu	Val	Asn	Phe	Glu	Asp
2165						2170					2175			
Ser	Lys	Ile	Gln	Tyr	Ile	Asn	Lys	Ala	Leu	Lys	Lys	Asn	Ala	Asn
2180						2185					2190			
Lys	Ile	Phe	Gly	Lys	Asn	Thr	Val	Asn	Arg	Asp	Glu	Phe	Glu	Thr
2195						2200					2205			
Met	Lys	Arg	Asp	Ala	Gln	Gln	Asn	Ile	Arg	Asp	Leu	Lys	Ala	Gly
2210						2215					2220			
Ile	Gln	Thr	Ala	Ser	Gly	Glu	Ile	Ala	Thr	Ser	Met	Ile	Asp	Gln
2225						2230					2235			
Ile	Leu	Asp	Glu	Tyr	Glu	Asp	Arg	Val	Gly	Lys	Val	Ser	Ala	Lys
2240						2245					2250			
Ile	Glu	Lys	Met	Gly	Lys	Gln	Lys	Glu	Lys	Leu	Asp	Leu	Ala	Asp

2255		2260		2265
Asn Lys Gln Ala Leu Lys Ser Ser Ser Leu Ser Arg Gln Gln Ala				
2270		2275		2280
Lys Asp Ser Lys Ser Leu Ala Ser Tyr Ile Asn Phe Tyr Ile Lys				
2285		2290		2295
Gln Leu Glu Arg Gln Leu Lys Leu Thr Gly Lys Asn His Glu Leu				
2300		2305		2310
Gln Gln Lys Val Lys Glu Gln Ile Lys Glu Met Lys Val Ala Tyr				
2315		2320		2325
Asp Asp Ala Thr Leu Ala Ala His Gln Tyr Ile Thr Glu Ala Ala				
2330		2335		2340
Glu Val Asp Thr Glu Arg Gln Leu Gln Leu Asn Ala Asn Arg Leu				
2345		2350		2355
Arg Asp Ala Gln Asn Glu Leu Ser Lys Ala Asp Tyr Lys Ala Gly				
2360		2365		2370
Phe Ile Ser Gln Glu Tyr Gln Ile Asp Leu Tyr Arg Lys Asn Gln				
2375		2380		2385
Glu Ala Lys Phe Lys Gly Tyr Leu Lys Glu Lys Glu Ala Leu Glu				
2390		2395		2400
Gln Asn Lys Ser Glu Leu Gln Asp Met Tyr Glu Ile Tyr Lys Ser				
2405		2410		2415
Val Pro Thr Gln Ala Gln Lys Ile Lys Glu Ala Leu Ile Glu Thr				
2420		2425		2430
Lys Asn Ala Ile Arg Asp Asn Asn Lys Gly Leu Tyr Asp Leu Lys				
2435		2440		2445
Tyr Asp Met Ala Asn Ser Val Ile Asn Gln Ile Lys Asp Ile Tyr				
2450		2455		2460
Ser Lys Gln Leu Glu Val Ala Thr Lys Ala Tyr Asp Asp Glu Tyr				
2465		2470		2475
Lys Ala Tyr Glu Lys Met Ile Asn Lys Lys Leu Lys Leu Ile Asp				
2480		2485		2490

Asp	Glu	Gln	Thr	Gln	Glu	Ser	Phe	Asn	Lys	Asp	Val	Arg	Asp	Arg
2495						2500					2505			
Thr	Glu	Ala	Met	Asp	Lys	Ile	Arg	Asp	Glu	Ile	Ala	Gln	Arg	Ser
2510						2515					2520			
Gly	Asp	Asp	Ser	Leu	Ala	Asn	Gln	Lys	Lys	Leu	Lys	Asp	Leu	Arg
2525						2530					2535			
Glu	Gln	Leu	Lys	Gln	Gln	Glu	Glu	Asp	Tyr	Thr	Met	Phe	Ile	Asn
2540						2545					2550			
Asn	Lys	Asn	Arg	Asp	Asp	Arg	Arg	Lys	Ala	Leu	Gln	Asp	Glu	Leu
2555						2560					2565			
Asn	Asp	Lys	Asn	Glu	Gln	Ile	Gln	Glu	Gln	Lys	Glu	Asp	Leu	Asn
2570						2575					2580			
Lys	Ala	Phe	Gln	Asp	Leu	Ile	Gly	Asp	Thr	Arg	Arg	Phe	Asn	Ala
2585						2590					2595			
Ile	Gln	Glu	Ser	Leu	Met	Glu	Gly	Gln	Ile	Asp	Lys	Tyr	Lys	Ser
2600						2605					2610			
Leu	Ile	Ala	Asp	Leu	Thr	Lys	Tyr	Val	Asn	Asp	Asn	Met	Lys	Glu
2615						2620					2625			
Ile	Gly	Arg	Ser	Thr	Ser	Glu	Gly	Ile	Leu	Asp	Gly	Leu	Ala	Ala
2630						2635					2640			
Ser	Phe	Lys	Gly	Leu	Ser	Ser	Leu	Ser	Lys	Glu	Leu	Gln	Lys	Gln
2645						2650					2655			
Glu	Lys	Asn	Asn	Leu	Asn	Pro	Val	Pro	Asn	Ser	Lys	Leu	Lys	Pro
2660						2665					2670			
Thr	Lys	Val	Asp	Glu	Ala	Thr	Ile	Ala	Ala	Ile	Lys	Lys	Val	Asn
2675						2680					2685			
Gly	Leu	Ser	Pro	Thr	Thr	Ile	Leu	Gln	Gly	Leu	Asp	Ile	Lys	Pro
2690						2695					2700			
Val	Asn	Leu	Pro	Lys	Asp	Val	Lys	Pro	Ser	Lys	Thr	Val	Thr	Asn
2705						2710					2715			

Asn Asn Lys Thr Thr Ala Lys Ala Leu Val Asn Ile Glu Asn Phe
2720 2725 2730

Asn Gly Thr Lys Ala Glu Ala Asp Lys Leu Ala Asn Asn Leu Ala
2735 2740 2745

Thr Ala Met Arg Lys Gln Gly Val Leu
2750 2755

<210> 39
<211> 319
<212> PRT
<213> Staphylococcus epidermidis

<400> 39

Met Ala Glu Thr Lys Lys Gln Phe Glu Asn Lys Val Ser Val Thr Gly
1 5 10 15

Thr Leu Lys Ser Leu Glu Val Thr Asp Leu Val Thr Ala Lys Lys Val
20 25 30

Pro Met Lys Ile Ala Thr Leu Arg Ile Glu Thr Gly Lys Gly Glu Thr
35 40 45

His Thr Ala Lys Met Met Ala Val Lys His Phe Glu Arg Asp Gly Val
50 55 60

Lys Thr Glu Asn Lys Ser Tyr Ser Ala Ile Glu Thr Met Gln Lys Glu
65 70 75 80

Tyr Val Ser Ile Glu Asp Ile Ser Glu Asn Lys Ala Gly Glu Asp Ala
85 90 95

Glu Ala Thr Val Val Asn Val Asn Gly Ser Met Ser Ile Asn Met Tyr
100 105 110

Lys Asn Lys Ala Glu Lys Val Val Glu Thr Asn Gln Ile Glu Ala Arg
115 120 125

Phe Val Asn Arg Val Lys Asp Val Glu Asn Ala Gln Phe Gly Ala Glu
130 135 140

Phe Thr Leu Gln Thr Tyr Leu Ile Ser Lys Gly Gln Arg Val Ile Lys
145 150 155 160

Asn Glu Glu Glu Thr Asp Glu Val Thr Phe Lys Ala Ala Thr Ile Asp

165

170

175

Tyr Arg Gly Gln Ala His Pro Phe Glu Phe Thr Ala Asn Asp Glu Tyr
 180 185 190

Gly Val Ala Glu Trp Ile Glu Asp Glu Val Glu Leu Gly Gln Ser Leu
 195 200 205

Ile Leu Gln Gly Leu Ile Ile Asn Lys Phe Ile Val Glu Gln Val Glu
 210 215 220

Arg Ser Ser Ser Ala Gly Ile Gly Lys Ala Ile Val Asp Thr Arg Arg
 225 230 235 240

Glu Val Glu Arg Lys Leu Leu Val Glu Gly Ile Ile Pro Ile Glu Asp
 245 250 255

Glu Asp Asp Pro Lys Tyr Ile Thr Glu Glu Glu Ile Lys Glu Ala Asn
 260 265 270

Lys Lys Tyr Glu Asp Lys Lys Thr Glu Val Glu Ala Ser Thr Asn Gly
 275 280 285

Thr Lys Lys Thr Glu Val Lys Lys Gly Val Ala Thr Ser Lys Pro Lys
 290 295 300

Ala Ala Lys Pro Thr Ile Glu Ile Asp Asp Asp Asp Leu Pro Phe
 305 310 315

<210> 40

<211> 797

<212> PRT

<213> Staphylococcus epidermidis

<400> 40

Leu Pro Gln Ala Lys Lys Arg Thr Ser Thr Lys Arg Lys Gly Asn Lys
 1 5 10 15

Lys Thr Asn Lys Lys Lys Gln Asn Glu Thr Pro Leu Arg Tyr Ile Phe
 20 25 30

Ser Ile Ile Val Val Ile Leu Ile Ile Leu Gly Ala Phe Gln Leu Gly
 35 40 45

Ile Ile Gly Arg Met Ile Asp Ser Phe Phe Asn Tyr Leu Phe Gly Met
 50 55 60

Ser Arg Tyr Leu Thr Tyr Ile Leu Val Leu Ile Ala Thr Ile Phe Ile
65 70 75 80

Thr Tyr Ser Lys Gln Ile Pro Arg Thr Arg Arg Ser Ile Gly Ala Ile
85 90 95

Val Leu Gln Leu Ala Leu Leu Phe Ile Ala Gln Leu Tyr Phe His Phe
100 105 110

Ser His Asn Ile Thr Ser Gln Arg Glu Pro Val Leu Ser Phe Val Tyr
115 120 125

Lys Ala Tyr Glu Gln Thr His Phe Pro Asn Phe Gly Gly Gly Leu Ile
130 135 140

Gly Phe Tyr Leu Leu Lys Leu Phe Ile Pro Leu Ile Ser Ile Val Gly
145 150 155 160

Val Ile Ile Ile Thr Ile Leu Leu Leu Ala Ser Ser Phe Ile Leu Leu
165 170 175

Leu Asn Leu Arg His Arg Asp Val Thr Lys Ser Leu Phe Asp Asn Leu
180 185 190

Lys Ser Ser Ser Asn His Ala Ser Glu Ser Ile Lys Gln Lys Arg Glu
195 200 205

Gln Asn Lys Ile Lys Lys Glu Glu Lys Ala Gln Leu Lys Glu Ala Lys
210 215 220

Ile Glu Arg Lys Lys Gln Lys Lys Ser Arg Gln Asn Asn Asn Val Ile
225 230 235 240

Lys Asp Val Ser Asp Phe Pro Glu Ile Ser Gln Ser Asp Asp Ile Pro
245 250 255

Ile Tyr Gly His Asn Glu Gln Glu Asp Lys Arg Pro Asn Thr Ala Asn
260 265 270

Gln Arg Gln Lys Arg Val Leu Asp Asn Glu Gln Phe Gln Gln Ser Leu
275 280 285

Pro Ser Thr Lys Asn Gln Ser Ile Asn Asn Asn Gln Pro Ser Thr Thr
290 295 300

Ala Glu Asn Asn Gln Gln Gln Ser Gln Ala Glu Gly Ser Ile Ser Glu
305 310 315 320

Ala Gly Glu Glu Ala Asn Ile Glu Tyr Thr Val Pro Pro Leu Ser Leu
325 330 335

Leu Lys Gln Pro Thr Lys Gln Lys Thr Thr Ser Lys Ala Glu Val Gln
340 345 350

Arg Lys Gly Gln Val Leu Glu Ser Thr Leu Lys Asn Phe Gly Val Asn
355 360 365

Ala Lys Val Thr Gln Ile Lys Ile Gly Pro Ala Val Thr Gln Tyr Glu
370 375 380

Ile Gln Pro Ala Gln Gly Val Lys Val Ser Lys Ile Val Asn Leu His
385 390 395 400

Asn Asp Ile Ala Leu Ala Leu Ala Ala Lys Asp Val Arg Ile Glu Ala
405 410 415

Pro Ile Pro Gly Arg Ser Ala Val Gly Ile Glu Val Pro Asn Asp Lys
420 425 430

Ile Ser Leu Val Thr Leu Lys Glu Val Leu Glu Asp Lys Phe Pro Ser
435 440 445

Lys Tyr Lys Leu Glu Val Gly Ile Gly Arg Asp Ile Ser Gly Asp Pro
450 455 460

Ile Ser Ile Gln Leu Asn Glu Met Pro His Leu Leu Val Ala Gly Ser
465 470 475 480

Thr Gly Ser Gly Lys Ser Val Cys Ile Asn Gly Ile Ile Thr Ser Ile
485 490 495

Leu Leu Asn Thr Lys Pro His Glu Val Lys Leu Met Leu Ile Asp Pro
500 505 510

Lys Met Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His Leu Leu Ile
515 520 525

Pro Val Val Thr Asn Pro His Lys Ala Ser Gln Ala Leu Glu Lys Ile
530 535 540

Val Ser Glu Met Glu Arg Arg Tyr Asp Leu Phe Gln His Ser Ser Thr

545		550		555		560
Arg Asn Ile Glu Gly Tyr Asn Gln Tyr Ile Arg Lys Gln Asn Glu Glu	565		570		575	
Leu Asp Glu Lys Gln Pro Glu Leu Pro Tyr Ile Val Val Ile Val Asp	580		585		590	
Glu Leu Ala Asp Leu Met Met Val Ala Gly Lys Glu Val Glu Asn Ala	595		600		605	
Ile Gln Arg Ile Thr Gln Met Ala Arg Ala Ala Gly Ile His Leu Ile	610		615		620	
Val Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Ile Ile Lys	625		630		635	
Asn Asn Ile Pro Ser Arg Ile Ala Phe Ala Val Ser Ser Gln Thr Asp	645		650		655	
Ser Arg Thr Ile Ile Gly Ala Gly Gly Ala Glu Lys Leu Leu Gly Lys	660		665		670	
Gly Asp Met Leu Tyr Val Gly Asn Gly Glu Ser Thr Thr Thr Arg Ile	675		680		685	
Gln Gly Ala Phe Leu Ser Asp Gln Glu Val Gln Asp Val Val Asn Tyr	690		695		700	
Val Val Glu Gln Gln Lys Ala Asn Tyr Val Lys Glu Met Glu Pro Asp	705		710		715	
Ala Pro Val Asp Lys Ser Glu Met Lys Ser Glu Asp Ala Leu Tyr Asp	725		730		735	
Glu Ala Tyr Leu Phe Val Ile Glu Lys Gln Lys Ala Ser Thr Ser Leu	740		745		750	
Leu Gln Arg Gln Phe Arg Ile Gly Tyr Asn Arg Ala Ser Arg Leu Met	755		760		765	
Asp Asp Leu Glu Arg Asn Gln Val Ile Gly Pro Gln Lys Gly Ser Lys	770		775		780	
Pro Arg Gln Ile Leu Val Asp Leu Glu Asn Asp Glu Val	785		790		795	

<210> 41
<211> 429
<212> PRT
<213> Staphylococcus epidermidis

<400> 41

Met Lys Thr His Gln Tyr Glu Leu Ile Asp Glu Lys Val Phe Glu His
1 5 10 15

Glu Phe Asp Asn Gly Leu Lys Leu Phe Ile Ile Pro Lys Pro Gly Phe
20 25 30

Gln Lys Thr Tyr Val Thr Tyr Thr Thr Gln Phe Gly Ser Leu Asp Asn
35 40 45

His Phe Lys Pro Ile Gly Ser Gln Gln Phe Val Lys Val Pro Asp Gly
50 55 60

Val Ala His Phe Leu Glu His Lys Leu Phe Glu Lys Glu Asp Glu Asp
65 70 75 80

Leu Phe Thr Ala Phe Ala Glu Glu Asn Ala Gln Ala Asn Ala Phe Thr
85 90 95

Ser Phe Asp Arg Thr Ser Tyr Leu Phe Ser Ala Thr Ser Asn Ile Glu
100 105 110

Ser Asn Ile Lys Arg Leu Leu Asn Met Val Glu Thr Pro Tyr Phe Thr
115 120 125

Glu Glu Thr Val Asn Lys Glu Lys Gly Ile Ile Ala Glu Glu Ile Lys
130 135 140

Met Tyr Gln Glu Gln Pro Gly Tyr Lys Leu Met Phe Asn Thr Leu Arg
145 150 155 160

Ala Met Tyr Ser Lys His Pro Ile Arg Val Asp Ile Ala Gly Ser Val
165 170 175

Glu Ser Ile Tyr Glu Ile Thr Lys Asp Asp Leu Tyr Leu Cys Tyr Glu
180 185 190

Thr Phe Tyr His Pro Ser Asn Met Val Leu Phe Val Val Gly Asp Val
195 200 205

Ser Pro Gln Ser Ile Ile Lys Leu Val Glu Lys His Glu Asn Gln Arg
210 215 220

Asn Lys Thr Tyr Gln Pro Arg Ile Glu Arg Ala Gln Ile Asp Glu Pro
225 230 235 240

Arg Glu Ile Asn Gln Arg Phe Val Ser Glu Lys Met Lys Leu Gln Ser
245 250 255

Pro Arg Leu Met Leu Gly Phe Lys Asn Glu Pro Leu Asp Glu Ser Ala
260 265 270

Thr Lys Phe Val Gln Arg Asp Leu Glu Met Thr Phe Phe Tyr Glu Leu
275 280 285

Val Phe Gly Glu Glu Thr Glu Phe Tyr Gln Gln Leu Leu Asn Lys Asp
290 295 300

Leu Ile Asp Glu Thr Phe Gly Tyr Gln Phe Val Leu Glu Pro Ser Tyr
305 310 315 320

Ser Phe Ser Ile Ile Thr Ser Ala Thr Gln Gln Pro Asp Leu Phe Lys
325 330 335

Gln Leu Ile Met Asp Glu Leu Arg Lys Tyr Lys Gly Asn Leu Lys Asp
340 345 350

Gln Glu Ala Phe Asp Leu Leu Lys Lys Gln Phe Ile Gly Glu Phe Ile
355 360 365

Ser Ser Leu Asn Ser Pro Glu Tyr Ile Ala Asn Gln Tyr Ala Lys Leu
370 375 380

Tyr Phe Glu Gly Val Ser Val Phe Asp Met Leu Asp Ile Val Glu Asn
385 390 395 400

Ile Thr Leu Glu Ser Val Asn Glu Thr Ser Glu Leu Phe Leu Asn Phe
405 410 415

Asp Gln Leu Val Asp Ser Arg Leu Glu Met Glu Asn Arg
420 425

<210> 42

<211> 329

<212> PRT

<213> Staphylococcus epidermidis

<400> 42

Met Thr Glu Gln Lys Asp Ile Lys Glu Thr Glu Tyr Arg Arg Gln Lys
1 5 10 15

Gly Thr Thr Ser Thr Pro Ser Arg Arg Arg Asn Lys Lys Arg Met Arg
20 25 30

Lys Leu Pro Phe Ile Ile Leu Val Ile Leu Ile Ile Leu Ile Ser Ile
35 40 45

Ile Val Tyr Ile Thr His Gln Tyr Asn Ser Gly Met Lys Tyr Ala Lys
50 55 60

Glu His Ala Lys Asp Val Lys Val His Lys Phe Asn Gly Asn Met Lys
65 70 75 80

Asn Asp Gly Lys Ile Ser Val Leu Val Leu Gly Ala Asp Lys Ala Gln
85 90 95

Gly Gly Lys Ser Arg Thr Asp Ser Ile Met Ile Val Gln Tyr Asp Tyr
100 105 110

Val His Lys Lys Met Lys Met Met Ser Val Met Arg Asp Ile Tyr Ala
115 120 125

Asp Ile Pro Gly Tyr Asp Lys Tyr Lys Ile Asn Ala Ala Tyr Ser Leu
130 135 140

Gly Gly Pro Glu Leu Leu Arg Lys Thr Leu Asn Lys Asn Leu Gly Val
145 150 155 160

Asn Pro Glu Tyr Tyr Ala Val Val Asp Phe Thr Gly Phe Glu Lys Met
165 170 175

Ile Asp Glu Leu Gln Pro Asn Gly Val Pro Ile Asp Val Glu Lys Asp
180 185 190

Met Ser Glu Asn Ile Gly Val Ser Leu Lys Lys Gly His His Lys Leu
195 200 205

Asn Gly Lys Glu Leu Leu Gly Tyr Ala Arg Phe Arg His Asp Pro Glu
210 215 220

Gly Asp Phe Gly Arg Val Arg Arg Gln Gln Gln Val Met Gln Thr Leu
225 230 235 240

Lys Gln Glu Leu Val Asn Phe Asn Thr Val Ala Lys Leu Pro Lys Val
245 250 255

Ala Gly Ile Leu Arg Gly Tyr Val Asn Thr Asn Met Pro Asn Ser Ala
260 265 270

Ile Phe Gln Thr Gly Ile Ser Phe Gly Ile Arg Gly Asp Lys Asp Val
275 280 285

Gln Ser Leu Thr Val Pro Ile Lys Gly Ser Tyr Gln Asp Ile Asn Thr
290 295 300

Asn Asn Asp Gly Ser Ala Leu Gln Ile Asp Ser Glu Lys Asn Lys Gln
305 310 315 320

Ala Ile Lys Asn Phe Phe Glu Asp Asn
325

<210> 43
<211> 627
<212> PRT
<213> Staphylococcus epidermidis

<400> 43

Met Glu Ala Tyr Lys Ile Glu His Leu Asn Lys Ser Tyr Ala Asp Lys
1 5 10 15

Glu Ile Phe Asn Asp Leu Asn Leu Ser Ile Ser Glu His Glu Arg Ile
20 25 30

Gly Leu Val Gly Ile Asn Gly Thr Gly Lys Ser Thr Leu Leu Lys Val
35 40 45

Ile Gly Gly Leu Asp Glu Asp Phe Thr Ala Asp Ile Thr His Pro Asn
50 55 60

Gln Tyr Arg Ile Arg Tyr Ser Ser Gln Lys Gln Asp Leu Asn Gly His
65 70 75 80

Met Thr Val Phe Glu Ala Val Leu Ser Ser Asp Thr Pro Thr Leu Arg
85 90 95

Ile Ile Lys Lys Tyr Glu Glu Ala Val Asn Arg Tyr Ala Leu Asp Gln
100 105 110

Ser Asp Ser Asn Phe Asn Lys Met Met Glu Ala Gln Glu Glu Met Asp

115					120					125					
Gln	Lys	Asp	Ala	Trp	Asp	Tyr	Asn	Ala	Glu	Ile	Lys	Thr	Ile	Leu	Ser
130					135					140					
Lys	Leu	Gly	Ile	His	Asp	Thr	Thr	Lys	Lys	Ile	Val	Glu	Leu	Ser	Gly
145					150					155					160
Gly	Gln	Gln	Lys	Arg	Val	Val	Leu	Ala	Lys	Thr	Leu	Ile	Glu	Gln	Pro
165					170					175					
Asp	Leu	Leu	Leu	Leu	Asp	Glu	Pro	Thr	Asn	His	Leu	Asp	Phe	Glu	Ser
180					185					190					
Ile	Arg	Trp	Leu	Ile	Asn	Tyr	Val	Lys	Gln	Tyr	Pro	His	Thr	Val	Leu
195					200					205					
Phe	Val	Thr	His	Asp	Arg	Tyr	Phe	Leu	Asn	Glu	Val	Ser	Thr	Arg	Ile
210					215					220					
Ile	Glu	Leu	Asp	Arg	Gly	Lys	Leu	Lys	Thr	Tyr	Pro	Gly	Asn	Tyr	Glu
225					230					235					240
Asp	Tyr	Ile	Val	Met	Arg	Ala	Glu	Asn	Glu	Leu	Val	Glu	Gln	Lys	Gln
245					250					255					
Gln	Glu	Lys	Gln	Lys	Ala	Leu	Tyr	Lys	Gln	Glu	Leu	Ala	Trp	Met	Arg
260					265					270					
Ala	Gly	Ala	Lys	Ala	Arg	Thr	Thr	Lys	Gln	Gln	Ala	Arg	Ile	Asn	Arg
275					280					285					
Phe	Asn	Gln	Leu	Glu	Ser	Asp	Val	Lys	Thr	Gln	His	Thr	Gln	Asp	Lys
290					295					300					
Gly	Glu	Leu	Asn	Leu	Ala	Tyr	Ser	Arg	Leu	Gly	Lys	Gln	Val	Tyr	Glu
305					310					315					320
Leu	Lys	Asn	Leu	Ser	Lys	Ser	Ile	Asn	Asn	Lys	Val	Leu	Phe	Glu	Asp
325					330					335					
Val	Thr	Glu	Ile	Ile	Gln	Ser	Gly	Arg	Arg	Ile	Gly	Ile	Val	Gly	Pro
340					345					350					
Asn	Gly	Ala	Gly	Lys	Thr	Thr	Leu	Leu	Asn	Ile	Leu	Ser	Asn	Glu	Asp
355					360					365					

Gln Asp Tyr Glu Gly Glu Leu Lys Ile Gly Gln Thr Val Lys Val Ala
370 375 380

Tyr Phe Lys Gln Thr Glu Lys Thr Leu Asp Arg Asp Ile Arg Val Ile
385 390 395 400

Asp Tyr Leu Arg Glu Glu Ser Glu Met Ala Lys Glu Lys Asp Gly Thr
405 410 415

Ser Ile Ser Val Thr Gln Leu Leu Glu Arg Phe Leu Phe Pro Ser Ala
420 425 430

Thr His Gly Lys Lys Val Tyr Lys Leu Ser Gly Gly Glu Gln Lys Arg
435 440 445

Leu Tyr Leu Leu Arg Leu Leu Val His Lys Pro Asn Val Leu Leu Leu
450 455 460

Asp Glu Pro Thr Asn Asp Leu Asp Thr Glu Thr Leu Thr Ile Leu Glu
465 470 475 480

Asp Tyr Ile Asp Asp Phe Gly Gly Ser Val Ile Thr Val Ser His Asp
485 490 495

Arg Tyr Phe Leu Asn Lys Val Val Gln Glu Tyr Trp Phe Ile His Asp
500 505 510

Gly Lys Ile Glu Lys Ile Ile Gly Ser Phe Glu Asp Tyr Glu Ser Phe
515 520 525

Lys Lys Glu His Glu Arg Gln Ala Met Leu Ser Lys Gln Thr Glu Gln
530 535 540

Gln Asn Lys His Lys His Gln Pro Lys Lys Lys Thr Gly Leu Ser Tyr
545 550 555 560

Lys Glu Lys Leu Glu Tyr Glu Thr Ile Met Thr Arg Ile Glu Met Thr
565 570 575

Glu Thr Arg Leu Glu Asp Leu Glu Gln Glu Met Ile Asn Ala Ser Asp
580 585 590

Asn Tyr Ala Arg Ile Lys Glu Leu Asn Glu Glu Lys Glu Gln Leu Glu
595 600 605

Ala Thr Tyr Glu Ala Asp Ile Thr Arg Trp Ser Glu Leu Glu Glu Ile
610 615 620

Lys Glu Gln
625

<210> 44
<211> 270
<212> PRT
<213> Staphylococcus epidermidis

<400> 44

Met Lys Lys Leu Phe Gly Ile Ile Leu Val Leu Ala Leu Thr Ile Ala
1 5 10 15

Leu Ala Ala Cys Gly Gly Gly Lys Asp Lys Glu Lys Thr Ile Thr Val
20 25 30

Gly Ala Ser Pro Ala Pro His Ala Glu Ile Leu Glu Lys Ala Lys Pro
35 40 45

Leu Leu Lys Lys Lys Gly Tyr Asp Leu Lys Ile Lys Pro Ile Asn Asp
50 55 60

Tyr Thr Thr Pro Asn Lys Leu Leu Asp Lys Gly Glu Ile Asp Ala Asn
65 70 75 80

Phe Phe Gln His Thr Pro Tyr Leu Asn Thr Glu Ser Lys Glu Lys Gly
85 90 95

Tyr Lys Ile Glu Ser Ala Gly Asn Val Glu Leu Glu Pro Met Ala Val
100 105 110

Tyr Ser Lys Lys Tyr Lys Ser Leu Lys Asp Leu Pro Lys Gly Ala Thr
115 120 125

Val Tyr Val Ser Asn Asn Pro Ala Glu Gln Gly Arg Phe Leu Lys Phe
130 135 140

Phe Val Asp Glu Gly Leu Ile Lys Leu Lys Lys Gly Val Lys Ile Glu
145 150 155 160

Asn Ala Lys Phe Asp Asp Ile Thr Glu Asn Lys Lys Asp Ile Lys Phe
165 170 175

Asn Asn Lys Gln Ser Ala Glu Tyr Leu Pro Lys Ile Tyr Gln Asn Gln

180	185	190
Asp Ala Asp Ala Val Ile Ile Asn Ser Asn Tyr Ala Ile Asp Gln Lys		
195	200	205
Leu Ser Pro Lys Lys Asp Ser Ile Ala Leu Glu Ser Pro Lys Asp Asn		
210	215	220
Pro Tyr Ala Asn Leu Ile Ala Val Lys Lys Gly His Lys Asp Asp Lys		
225	230	235
Asn Ile Lys Val Leu Met Glu Val Leu Gln Ser Lys Glu Ile Gln Asp		
	245	250
		255
Tyr Ile Lys Asp Lys Tyr Asp Gly Ala Val Val Pro Ala Lys		
	260	265
		270
<210> 45		
<211> 439		
<212> PRT		
<213> Staphylococcus epidermidis		
<400> 45		
Met Glu Leu Thr Ile Tyr His Thr Asn Asp Ile His Ser His Leu Asn		
1	5	10
		15
Glu Tyr Ala Arg Ile Gln Ala Tyr Met Ala Lys His Arg Pro Gln Leu		
	20	25
		30
Glu His Pro Ser Leu Tyr Ile Asp Ile Gly Asp His Val Asp Leu Ser		
	35	40
		45
Ala Pro Val Thr Glu Ala Thr Val Gly His Lys Asn Ile Glu Leu Leu		
	50	55
		60
Asn Glu Ala His Cys Asp Ile Ala Thr Ile Gly Asn Asn Glu Gly Met		
65	70	75
		80
Thr Ile Ser His Asp Ala Leu Gln Asn Leu Tyr Asn Asp Ala Asp Phe		
	85	90
		95
Lys Val Ile Cys Thr Asn Val Ile Asp Glu Glu Gly His Leu Pro His		
	100	105
		110
His Ile Thr Ser Ser Tyr Ile Lys Glu Ile Lys Gly Thr Arg Ile Leu		
	115	120
		125

Phe Val Ala Ala Thr Ala Pro Phe Thr Pro Phe Tyr Arg Ala Leu Asp
130 135 140

Trp Ile Val Thr Asp Pro Leu Ala Ala Ile Lys Asp Glu Ile Asn Ala
145 150 155 160

His Gln Gly Glu Tyr Asp Leu Leu Met Val Met Ser His Val Gly Ile
165 170 175

Phe Phe Asp Glu Lys Leu Cys Gln Glu Ile Pro Glu Ile Asp Val Ile
180 185 190

Phe Gly Ser His Thr His His His Phe Glu His Gly Glu Ile Asn Asn
195 200 205

Gly Val Leu Met Ala Ala Ala Gly Lys Tyr Gly Tyr Tyr Leu Gly Glu
210 215 220

Val Asn Ile Thr Ile Glu Asn Gly Lys Ile Val Asp Lys Ile Ala Lys
225 230 235 240

Ile His Pro Ile Glu Thr Leu Pro Leu Val Glu Thr His Phe Glu Glu
245 250 255

Glu Gly Arg Ala Leu Leu Ser Lys Pro Val Val Asn His His Val Asn
260 265 270

Leu Val Lys Arg Thr Asp Val Val Thr Arg Thr Ser Tyr Leu Leu Ala
275 280 285

Glu Ser Val Tyr Glu Phe Ser Arg Ala Asp Cys Ala Ile Val Asn Ala
290 295 300

Gly Leu Ile Val Asn Gly Ile Glu Ala Asp Lys Val Thr Glu Tyr Asp
305 310 315 320

Ile His Arg Met Leu Pro His Pro Ile Asn Ile Val Arg Val Arg Leu
325 330 335

Thr Gly Lys Gln Leu Lys Gln Val Ile Gln Lys Ser Gln Lys Gln Glu
340 345 350

Tyr Met His Glu His Ala Gln Gly Leu Gly Phe Arg Gly Asp Ile Phe
355 360 365

Gly Gly Tyr Ile Leu Tyr Asn Leu Gly Phe Ile Glu Ser Glu Asp Arg
370 375 380

Tyr Phe Ile Gly Asp Glu Glu Ile Gln Asn Asp Lys Gln Tyr Thr Leu
385 390 395 400

Gly Thr Val Asp Met Tyr Thr Phe Gly Arg Tyr Phe Pro Leu Leu Lys
405 410 415

Gly Leu Ser Thr Asp Tyr Ile Met Pro Glu Phe Leu Arg Asp Ile Phe
420 425 430

Lys Glu Lys Leu Leu Lys Leu
435

<210> 46
<211> 203
<212> PRT
<213> Staphylococcus epidermidis

<400> 46

Met Glu Lys Val Ile Tyr Leu Ala Gly His Ile Leu Asn Glu Ala Met
1 5 10 15

Val Asp Tyr Arg Glu Lys Gln His Asn Gln Val Glu Ala Ile Glu Gly
20 25 30

Val Lys Pro Tyr Ser Pro His Gln Asp Lys Ser Ile Asn Asp Lys Ser
35 40 45

Asn Ala Val Gln Glu Gly Leu Ala Glu Arg Ile Leu Lys Asn Asp Phe
50 55 60

Thr Ala Met Glu Lys Ser Asp Ile Tyr Val Leu Asp Val Leu Asn Glu
65 70 75 80

Gly Leu Gly Thr Ile Ser Glu Leu Gly Ile Ile Ile Gly Met Lys Lys
85 90 95

Gln Ala Gln Lys Thr Ile Asp Arg Leu Ser Val Leu Ser Glu Glu Ile
100 105 110

Lys His Asp Val Tyr Gly Asp Gln Thr Glu Ala Tyr Asp Leu Ile Gln
115 120 125

Asp Glu Ile Tyr Lys Gln Glu Lys Ile Leu Asn Lys Thr Val Leu Cys
130 135 140

Tyr Cys Ser Asp Ile Arg Gln Gly His Gly Lys Pro Tyr Thr Asp Pro
145 150 155 160

Asp Arg Ala Glu Phe Ser Thr Asn Gln Phe Val Tyr Gly Met Val Leu
165 170 175

Glu Ala Thr Asn Gly Glu Gly Phe Ile Thr Trp Asp Gln Val Leu His
180 185 190

Arg Leu Asp Leu Phe Gly Ser Gly Leu Ile Val
195 200

<210> 47
<211> 59
<212> PRT
<213> Staphylococcus epidermidis

<400> 47

Met Ser Lys Lys Phe Arg Val Glu Asp Lys Glu Thr Ile Ala Asp Cys
1 5 10 15

Leu Asp Arg Met Lys Lys Glu Gly Phe Met Pro Ile Arg Arg Ile Glu
20 25 30

Lys Pro Val Tyr Lys Glu Asn Lys Asp Gly Ser Ile Glu Ile Leu Lys
35 40 45

Gln Asp Ile Ile Phe Val Gly Ala Leu Ile Gln
50 55

<210> 48
<211> 3692
<212> PRT
<213> Staphylococcus epidermidis

<400> 48

Met Asn Leu Phe Arg Lys Gln Lys Phe Ser Ile Arg Lys Phe Asn Ile
1 5 10 15

Gly Ile Phe Ser Ala Leu Ile Ala Thr Val Ala Phe Leu Ala His Pro
20 25 30

Gly Gln Ala Thr Ala Ser Glu Leu Glu Pro Ser Gln Asn Asn Asp Thr
35 40 45

Thr Ala Gln Ser Asp Gly Gly Leu Glu Asn Thr Ser Gln Ser Asn Pro

50		55		60
Ile Ser Glu Glu Thr Thr Asn Thr Leu Ser Gly Gln Thr Val Pro Ser				
65		70		80
Ser Thr Glu Asn Lys Gln Thr Gln Asn Val Pro Asn His Asn Ala Gln				
	85		90	95
Pro Ile Ala Ile Asn Thr Glu Glu Ala Glu Ser Ala Gln Thr Ala Ser				
	100		105	110
Tyr Thr Asn Ile Asn Glu Asn Asn Asp Thr Ser Asp Asp Gly Leu His				
	115		120	125
Val Asn Gln Pro Ala Lys His His Ile Glu Ala Gln Ser Glu Asp Val				
	130		135	140
Thr Asn His Thr Asn Ser Asn His Ser Asn Ser Ser Ile Pro Glu Asn				
145		150		155
Lys Ala Thr Thr Glu Ser Ser Ser Lys Pro Lys Lys Arg Gly Lys Arg				
	165		170	175
Ser Leu Asp Thr Asn Asn Gly Asn Asp Thr Thr Ser Thr Thr Gln Asn				
	180		185	190
Thr Asp Pro Asn Leu Ser Asn Thr Gly Pro Asn Gly Ile Asn Thr Val				
	195		200	205
Ile Thr Phe Asp Asp Leu Gly Ile Lys Thr Ser Thr Asn Arg Ser Arg				
210		215		220
Pro Glu Val Lys Val Val Asp Ser Leu Asn Gly Phe Thr Met Val Asn				
225		230		235
Gly Gly Lys Val Gly Leu Leu Asn Ser Val Leu Glu Arg Thr Ser Val				
	245		250	255
Phe Asp Ser Ala Asp Pro Lys Asn Tyr Gln Ala Ile Asp Asn Val Val				
	260		265	270
Ala Leu Gly Arg Ile Lys Gly Asn Asp Pro Asn Asp His Asp Gly Phe				
	275		280	285
Asn Gly Ile Glu Lys Glu Phe Ser Val Asn Pro Asn Ser Glu Ile Ile				
290		295		300

Phe Ser Phe Asn Thr Met Thr Ala Lys Asn Arg Lys Gly Gly Thr Gln
305 310 315 320

Leu Val Leu Arg Asn Ala Glu Asn Asn Gln Glu Ile Ala Ser Thr Asp
325 330 335

Ile Gln Gly Gly Gly Val Tyr Arg Leu Phe Lys Leu Pro Asp Asn Val
340 345 350

His Arg Leu Lys Val Gln Phe Leu Pro Met Asn Glu Ile His Ser Asp
355 360 365

Phe Lys Arg Ile Gln Gln Leu His Asp Gly Tyr Arg Tyr Tyr Ser Phe
370 375 380

Ile Asp Thr Ile Gly Val Asn Ser Gly Ser His Leu Tyr Val Lys Ser
385 390 395 400

Arg Gln Val Asn Lys Asn Val Lys Asn Gly Lys Glu Phe Glu Val Asn
405 410 415

Thr Arg Ile Glu Asn Asn Gly Asn Phe Ala Ala Ala Ile Gly Gln Asn
420 425 430

Glu Leu Thr Tyr Lys Val Thr Leu Pro Glu Asn Phe Glu Tyr Val Asp
435 440 445

Asn Ser Thr Glu Val Ser Phe Val Asn Gly Asn Val Pro Asn Ser Thr
450 455 460

Val Asn Pro Phe Ser Val Asn Phe Asp Arg Gln Asn His Thr Leu Thr
465 470 475 480

Phe Ser Ser Asn Gly Leu Asn Leu Gly Arg Ser Ala Gln Asp Val Ala
485 490 495

Arg Phe Leu Pro Asn Lys Ile Leu Asn Ile Arg Tyr Lys Leu Arg Pro
500 505 510

Val Asn Ile Ser Thr Pro Arg Glu Val Thr Phe Asn Glu Ala Ile Lys
515 520 525

Tyr Lys Thr Phe Ser Glu Tyr Tyr Ile Asn Thr Asn Asp Asn Thr Val
530 535 540

Thr Gly Gln Gln Thr Pro Phe Ser Ile Asn Val Ile Met Asn Lys Asp
545 550 555 560

Asp Leu Ser Glu Gln Val Asn Lys Asp Ile Ile Pro Ser Asn Tyr Thr
565 570 575

Leu Ala Ser Tyr Asn Lys Tyr Asn Lys Leu Lys Glu Arg Ala Gln Thr
580 585 590

Val Leu Asp Glu Glu Thr Asn Asn Thr Pro Phe Asn Gln Arg Tyr Ser
595 600 605

Gln Thr Gln Ile Asp Asp Leu Leu His Glu Leu Gln Thr Thr Leu Ile
610 615 620

Asn Arg Val Ser Ala Ser Arg Glu Ile Asn Asp Lys Ala Gln Glu Met
625 630 635 640

Thr Asp Ala Val Tyr Asp Ser Thr Glu Leu Thr Thr Glu Glu Lys Asp
645 650 655

Thr Leu Val Asp Gln Ile Glu Asn His Lys Asn Glu Ile Ser Asn Asn
660 665 670

Ile Asp Asp Glu Leu Thr Asp Asp Gly Val Glu Arg Val Lys Glu Ala
675 680 685

Gly Leu His Thr Leu Glu Ser Asp Thr Pro His Pro Val Thr Lys Pro
690 695 700

Asn Ala Arg Gln Val Val Asn Asn Arg Ala Asp Gln Gln Lys Thr Leu
705 710 715 720

Ile Arg Asn Asn His Glu Ala Thr Thr Glu Glu Gln Asn Glu Ala Ile
725 730 735

Arg Gln Val Glu Ala His Ser Ser Asp Ala Ile Ala Lys Ile Gly Glu
740 745 750

Ala Glu Thr Asp Thr Thr Val Asn Glu Ala Arg Asp Asn Gly Thr Lys
755 760 765

Leu Ile Ala Thr Asp Val Pro Asn Pro Thr Lys Lys Ala Glu Ala Arg
770 775 780

Ala Ala Val Thr Asn Ser Ala Asn Ser Lys Ile Lys Asp Ile Asn Asn
785 790 795 800

Asn Thr Gln Ala Thr Leu Asp Glu Arg Asn Asp Ala Ile Ala Leu Val
805 810 815

Asn Arg Ser Lys Asp Glu Ala Ile Gln Asn Ile Asn Thr Ala Gln Gly
820 825 830

Asn Asp Asp Val Thr Glu Ala Gln Asn Asn Gly Thr Asn Thr Ile Gln
835 840 845

Gln Val Pro Leu Thr Pro Val Lys Arg Gln Asn Ala Ile Ala Thr Ile
850 855 860

Asn Ala Lys Ala Asp Glu Gln Lys Arg Leu Ile Gln Ala Asn Asn Asn
865 870 875 880

Ala Thr Thr Glu Glu Lys Ala Asp Ala Glu Arg Lys Val Asn Glu Ala
885 890 895

Val Ile Thr Ala Asn Gln Asn Ile Thr Asn Ala Thr Thr Asn Arg Asp
900 905 910

Val Asp Gln Ala Gln Thr Thr Gly Ser Gly Ile Ile Ser Ala Ile Ser
915 920 925

Pro Ala Thr Lys Ile Lys Glu Asp Ala Arg Ala Val Glu Ala Lys
930 935 940

Ala Ile Ala Gln Asn Gln Gln Ile Asn Ser Asn Asn Met Ala Thr Thr
945 950 955 960

Glu Glu Lys Glu Asp Ala Leu Asn Gln Val Glu Ala His Lys Gln Ala
965 970 975

Ala Ile Ala Thr Ile Asn Gln Ala Gln Ser Thr Gln Gln Val Ser Glu
980 985 990

Ala Lys Asn Asn Gly Ile Asn Thr Ile Asn Gln Asp Gln Pro Asn Ala
995 1000 1005

Val Lys Lys Asn Asn Thr Lys Ile Ile Leu Glu Gln Lys Gly Asn
1010 1015 1020

Glu Lys Lys Ser Ala Ile Ala Gln Thr Pro Asp Ala Thr Thr Glu

1025		1030		1035
Glu Lys Gln Glu Ala Val Ser Ala Val Ser Gln Ala Val Thr Asn				
1040		1045		1050
Gly Ile Thr His Ile Asn Gln Ala Asn Ser Asn Asp Asp Val Asp				
1055		1060		1065
Gln Glu Leu Ser Asn Ala Glu Gln Ile Ile Thr Gln Thr Asn Val				
1070		1075		1080
Asn Val Gln Lys Lys Pro Gln Ala Arg Gln Ala Leu Ile Ala Lys				
1085		1090		1095
Thr Asn Glu Arg Gln Ser Thr Ile Asn Thr Asp Asn Glu Gly Thr				
1100		1105		1110
Ile Glu Glu Lys Gln Lys Ala Ile Gln Ser Leu Asn Asp Ala Lys				
1115		1120		1125
Asn Leu Ala Asp Glu Gln Ile Thr Gln Ala Ala Ser Asn Gln Asn				
1130		1135		1140
Val Asp Asn Ala Leu Asn Ile Gly Ile Ser Asn Ile Ser Lys Ile				
1145		1150		1155
Gln Thr Asn Phe Thr Lys Lys Gln Gln Ala Arg Asp Gln Val Asn				
1160		1165		1170
Gln Lys Phe Gln Glu Lys Glu Ala Glu Leu Asn Ser Thr Pro His				
1175		1180		1185
Ala Thr Gln Asp Glu Lys Gln Asp Ala Leu Thr Arg Leu Thr Gln				
1190		1195		1200
Ala Lys Glu Thr Ala Leu Asn Asp Ile Asn Gln Ala Gln Thr Asn				
1205		1210		1215
Gln Asn Val Asp Thr Ala Leu Thr Ser Gly Ile Gln Asn Ile Gln				
1220		1225		1230
Asn Thr Gln Val Asn Val Arg Lys Lys Gln Glu Ala Lys Thr Thr				
1235		1240		1245
Ile Asn Asp Ile Val Gln Gln His Lys Gln Thr Ile Gln Asn Asn				
1250		1255		1260

Asp	Asp	Ala	Thr	Thr	Glu	Glu	Lys	Glu	Val	Ala	Asn	Asn	Leu	Val
1265						1270					1275			
Asn	Ala	Ser	Gln	Gln	Asn	Val	Ile	Ser	Lys	Ile	Asp	Asn	Ala	Thr
1280						1285					1290			
Thr	Asn	Asn	Gln	Ile	Asp	Gly	Ile	Val	Ser	Asp	Gly	Arg	Gln	Ser
1295						1300					1305			
Ile	Asn	Ala	Ile	Thr	Pro	Asp	Thr	Ser	Ile	Lys	Arg	Asn	Ala	Lys
1310						1315					1320			
Asn	Asp	Ile	Asp	Ile	Lys	Ala	Ala	Asp	Lys	Lys	Ile	Lys	Ile	Gln
1325						1330					1335			
Arg	Ile	Asn	Asp	Ala	Thr	Asp	Glu	Glu	Ile	Gln	Glu	Ala	Asn	Arg
1340						1345					1350			
Lys	Ile	Glu	Glu	Ala	Lys	Ile	Glu	Ala	Lys	Asp	Asn	Ile	Gln	Arg
1355						1360					1365			
Asn	Ser	Thr	Arg	Asp	Gln	Val	Asn	Glu	Ala	Lys	Thr	Asn	Gly	Ile
1370						1375					1380			
Asn	Lys	Ile	Glu	Asn	Ile	Thr	Pro	Ala	Thr	Thr	Val	Lys	Ser	Glu
1385						1390					1395			
Ala	Arg	Gln	Ala	Val	Gln	Asn	Lys	Ala	Asn	Glu	Gln	Ile	Asn	His
1400						1405					1410			
Ile	Gln	Asn	Thr	Pro	Asp	Ala	Thr	Asn	Glu	Glu	Lys	Gln	Glu	Ala
1415						1420					1425			
Ile	Asn	Arg	Val	Ser	Ala	Glu	Leu	Ala	Arg	Val	Gln	Ala	Gln	Ile
1430						1435					1440			
Asn	Ala	Glu	His	Thr	Thr	Gln	Gly	Val	Lys	Thr	Ile	Lys	Asp	Asp
1445						1450					1455			
Ala	Ile	Thr	Ser	Leu	Ser	Arg	Ile	Asn	Ala	Gln	Val	Val	Glu	Lys
1460						1465					1470			
Glu	Ser	Ala	Arg	Asn	Ala	Ile	Glu	Gln	Lys	Ala	Thr	Gln	Gln	Thr
1475						1480					1485			

Gln	Phe	Ile	Asn	Asn	Asn	Asp	Asn	Ala	Thr	Asp	Glu	Glu	Lys	Glu
1490						1495					1500			
Val	Ala	Asn	Asn	Leu	Val	Ile	Ala	Thr	Lys	Gln	Lys	Ser	Leu	Asp
1505						1510					1515			
Asn	Ile	Asn	Ser	Leu	Ser	Ser	Asn	Asn	Asp	Val	Glu	Asn	Ala	Lys
1520						1525					1530			
Val	Ala	Gly	Ile	Asn	Glu	Ile	Ala	Asn	Val	Leu	Pro	Ala	Thr	Ala
1535						1540					1545			
Val	Lys	Ser	Lys	Ala	Lys	Lys	Asp	Ile	Asp	Gln	Lys	Leu	Ala	Gln
1550						1555					1560			
Gln	Ile	Asn	Gln	Ile	Gln	Thr	His	Gln	Thr	Ala	Thr	Thr	Glu	Glu
1565						1570					1575			
Lys	Glu	Ala	Ala	Ile	Gln	Leu	Ala	Asn	Gln	Lys	Ser	Asn	Glu	Ala
1580						1585					1590			
Arg	Thr	Ala	Ile	Gln	Asn	Glu	His	Ser	Asn	Asn	Gly	Val	Ala	Gln
1595						1600					1605			
Ala	Lys	Ser	Asn	Gly	Ile	His	Glu	Ile	Glu	Leu	Val	Met	Pro	Asp
1610						1615					1620			
Ala	His	Lys	Lys	Ser	Asp	Ala	Lys	Gln	Ser	Ile	Asp	Asn	Lys	Tyr
1625						1630					1635			
Asn	Glu	Gln	Ser	Asn	Thr	Ile	Asn	Thr	Thr	Pro	Asp	Ala	Thr	Asp
1640						1645					1650			
Glu	Glu	Lys	Gln	Lys	Ala	Leu	Asp	Lys	Leu	Lys	Ile	Ala	Lys	Asp
1655						1660					1665			
Ala	Gly	Tyr	Asn	Lys	Val	Asp	Gln	Ala	Gln	Thr	Asn	Gln	Gln	Val
1670						1675					1680			
Ser	Asp	Ala	Lys	Thr	Glu	Ala	Ile	Asp	Thr	Ile	Thr	Asn	Ile	Gln
1685						1690					1695			
Ala	Asn	Val	Ala	Lys	Lys	Pro	Ser	Ala	Arg	Val	Glu	Leu	Asp	Ser
1700						1705					1710			

Lys	Phe	Glu	Asp	Leu	Lys	Arg	Gln	Ile	Asn	Ala	Thr	Pro	Asn	Ala
1715						1720					1725			
Thr	Glu	Glu	Glu	Lys	Gln	Asp	Ala	Ile	Gln	Arg	Leu	Asn	Gly	Lys
1730						1735					1740			
Arg	Asp	Glu	Val	Lys	Asn	Leu	Ile	Asn	Gln	Asp	Arg	Arg	Asp	Asn
1745						1750					1755			
Glu	Val	Glu	Gln	His	Lys	Asn	Ile	Gly	Leu	Gln	Glu	Leu	Glu	Thr
1760						1765					1770			
Ile	His	Ala	Asn	Pro	Thr	Arg	Lys	Ser	Asp	Ala	Leu	Gln	Glu	Leu
1775						1780					1785			
Gln	Thr	Lys	Phe	Ile	Ser	Gln	Thr	Glu	Leu	Ile	Asn	Asn	Asn	Lys
1790						1795					1800			
Asp	Ala	Thr	Asn	Glu	Glu	Lys	Asp	Glu	Ala	Lys	Arg	Leu	Leu	Glu
1805						1810					1815			
Ile	Ser	Lys	Asn	Lys	Thr	Ile	Thr	Asn	Ile	Asn	Gln	Ala	Gln	Thr
1820						1825					1830			
Asn	Asn	Gln	Val	Asp	Asn	Ala	Lys	Asp	Asn	Gly	Met	Asn	Glu	Ile
1835						1840					1845			
Ala	Thr	Ile	Ile	Pro	Ala	Thr	Thr	Ile	Lys	Thr	Asp	Ala	Lys	Thr
1850						1855					1860			
Ala	Ile	Asp	Lys	Lys	Ala	Glu	Gln	Gln	Val	Thr	Ile	Ile	Asn	Gly
1865						1870					1875			
Asn	Asn	Asp	Ala	Thr	Asp	Glu	Glu	Lys	Ala	Glu	Ala	Arg	Lys	Leu
1880						1885					1890			
Val	Glu	Lys	Ala	Lys	Ile	Glu	Ala	Lys	Ser	Asn	Ile	Thr	Asn	Ser
1895						1900					1905			
Asp	Thr	Glu	Arg	Glu	Val	Asn	Gly	Ala	Lys	Thr	Asn	Gly	Leu	Glu
1910						1915					1920			
Lys	Ile	Asn	Asn	Ile	Gln	Pro	Ser	Thr	Gln	Thr	Lys	Thr	Asn	Ala
1925						1930					1935			
Lys	Gln	Glu	Ile	Asn	Asp	Lys	Ala	Gln	Glu	Gln	Leu	Ile	Gln	Ile

1940	1945	1950
Asn Asn Thr Pro Asp Ala Thr 1955	Glu Glu Glu Lys Gln 1960	Glu Ala Thr 1965
Asn Arg Val Asn Ala Gly Leu 1970	Ala Gln Ala Ile 1975	Gln Asn Ile Asn 1980
Asn Ala His Ser Thr Gln Glu 1985	Val Asn Glu Ser 1990	Lys Thr Asn Ser 1995
Ile Ala Thr Ile Lys Ser Val 2000	Gln Pro Asn Val 2005	Ile Lys Lys Pro 2010
Thr Ala Ile Asn Ser Leu Thr 2015	Gln Glu Ala Asn 2020	Asn Gln Lys Thr 2025
Leu Ile Gly Asn Asp Gly Asn 2030	Ala Thr Asp Asp 2035	Glu Lys Glu Ala 2040
Ala Lys Gln Leu Val Thr Gln 2045	Lys Leu Asn Glu 2050	Gln Ile Gln Lys 2055
Ile His Glu Ser Thr Gln Asp 2060	Asn Gln Val Asp 2065	Asn Val Lys Ala 2070
Gln Ala Ile Thr Ala Ile Lys 2075	Leu Ile Asn Ala 2080	Asn Ala His Lys 2085
Arg Gln Asp Ala Ile Asn Ile 2090	Leu Thr Asn Leu 2095	Ala Glu Ser Lys 2100
Lys Ser Asp Ile Arg Ala Asn 2105	Gln Asp Ala Thr 2110	Thr Glu Glu Lys 2115
Asn Thr Ala Ile Gln Ser Ile 2120	Asp Asp Thr Leu 2125	Ala Gln Ala Arg 2130
Asn Asn Ile Asn Gly Ala Asn 2135	Thr Asn Ala Leu 2140	Val Asp Glu Asn 2145
Leu Glu Asp Gly Lys Gln Lys 2150	Leu Gln Arg Ile 2155	Val Leu Ser Thr 2160
Gln Thr Lys Thr Gln Ala Lys 2165	Ala Asp Ile Ala 2170	Gln Ala Ile Gly 2175

Gln	Gln	Arg	Ser	Thr	Ile	Asp	Gln	Asn	Gln	Asn	Ala	Thr	Thr	Glu
2180						2185					2190			
Glu	Lys	Gln	Glu	Ala	Leu	Glu	Arg	Leu	Asn	Gln	Glu	Thr	Asn	Gly
2195						2200					2205			
Val	Asn	Asp	Arg	Ile	Gln	Ala	Ala	Leu	Ala	Asn	Gln	Asn	Val	Thr
2210						2215					2220			
Asp	Glu	Lys	Asn	Asn	Ile	Leu	Glu	Thr	Ile	Arg	Asn	Val	Glu	Pro
2225						2230					2235			
Ile	Val	Ile	Val	Lys	Pro	Lys	Ala	Asn	Glu	Ile	Ile	Arg	Lys	Lys
2240						2245					2250			
Ala	Ala	Glu	Gln	Thr	Thr	Leu	Ile	Asn	Gln	Asn	Gln	Asp	Ala	Thr
2255						2260					2265			
Leu	Glu	Glu	Lys	Gln	Ile	Ala	Leu	Gly	Lys	Leu	Glu	Glu	Val	Lys
2270						2275					2280			
Asn	Glu	Ala	Leu	Asn	Gln	Val	Ser	Gln	Ala	His	Ser	Asn	Asn	Asp
2285						2290					2295			
Val	Lys	Ile	Val	Glu	Asn	Asn	Gly	Ile	Ala	Lys	Ile	Ser	Glu	Val
2300						2305					2310			
His	Pro	Glu	Thr	Ile	Ile	Lys	Arg	Asn	Ala	Lys	Gln	Glu	Ile	Glu
2315						2320					2325			
Gln	Asp	Ala	Gln	Ser	Gln	Ile	Asp	Thr	Ile	Asn	Ala	Asn	Asn	Lys
2330						2335					2340			
Ser	Thr	Asn	Glu	Glu	Lys	Ser	Ala	Ala	Ile	Asp	Arg	Val	Asn	Val
2345						2350					2355			
Ala	Lys	Ile	Asp	Ala	Ile	Asn	Asn	Ile	Thr	Asn	Ala	Thr	Thr	Thr
2360						2365					2370			
Gln	Leu	Val	Asn	Asp	Ala	Lys	Asn	Ser	Gly	Asn	Thr	Ser	Ile	Ser
2375						2380					2385			
Gln	Ile	Leu	Pro	Ser	Thr	Ala	Val	Lys	Thr	Asn	Ala	Leu	Ala	Ala
2390						2395					2400			

Leu	Ala	Ser	Glu	Ala	Lys	Asn	Lys	Asn	Ala	Ile	Ile	Asp	Gln	Thr
2405						2410						2415		
Pro	Asn	Ala	Thr	Ala	Glu	Glu	Lys	Glu	Glu	Ala	Asn	Asn	Lys	Val
2420						2425						2430		
Asp	Arg	Leu	Gln	Glu	Glu	Ala	Asp	Ala	Asn	Ile	Leu	Lys	Ala	His
2435						2440						2445		
Thr	Thr	Asp	Glu	Val	Asn	Asn	Ile	Lys	Asn	Gln	Ala	Val	Gln	Asn
2450						2455						2460		
Ile	Asn	Ala	Val	Gln	Val	Glu	Val	Ile	Lys	Lys	Gln	Asn	Ala	Lys
2465						2470						2475		
Asn	Gln	Leu	Asn	Gln	Phe	Ile	Asp	Asn	Gln	Lys	Lys	Ile	Ile	Glu
2480						2485						2490		
Asn	Thr	Pro	Asp	Ala	Thr	Leu	Glu	Glu	Lys	Ala	Glu	Ala	Asn	Arg
2495						2500						2505		
Leu	Leu	Gln	Asn	Val	Leu	Thr	Ser	Thr	Ser	Asp	Glu	Ile	Ala	Asn
2510						2515						2520		
Val	Asp	His	Asn	Asn	Glu	Val	Asp	Gln	Ala	Leu	Asp	Lys	Ala	Arg
2525						2530						2535		
Pro	Lys	Ile	Glu	Ala	Ile	Val	Pro	Gln	Val	Ser	Lys	Lys	Arg	Asp
2540						2545						2550		
Ala	Leu	Asn	Ala	Ile	Gln	Glu	Ala	Phe	Asn	Ser	Gln	Thr	Gln	Glu
2555						2560						2565		
Ile	Gln	Glu	Asn	Gln	Glu	Ala	Thr	Asn	Glu	Glu	Lys	Thr	Glu	Ala
2570						2575						2580		
Leu	Asn	Lys	Ile	Asn	Gln	Leu	Leu	Asn	Gln	Ala	Lys	Val	Asn	Ile
2585						2590						2595		
Asp	Gln	Ala	Gln	Ser	Asn	Lys	Asp	Val	Asp	Ser	Ala	Lys	Thr	Arg
2600						2605						2610		
Ser	Ile	Gln	Asp	Ile	Glu	Gln	Ile	Gln	Pro	His	Pro	Gln	Thr	Lys
2615						2620						2625		

Ala Thr	Gly Arg His Arg	Leu	Asn Glu Lys Ala	Asn	Gln Gln Gln
2630		2635		2640	
Ser Thr	Ile Ala Thr His	Pro	Asn Ser Thr Ile	Glu	Glu Arg Gln
2645		2650		2655	
Glu Ala	Ser Ala Lys Leu	Gln	Glu Val Leu Lys	Lys	Ala Ile Ala
2660		2665		2670	
Lys Ile	Asp Lys Gly Gln	Thr	Asn Asp Asp Val	Glu	Lys Thr Val
2675		2680		2685	
Val Asn	Gly Ile Ala Glu	Ile	Glu Asn Ile Leu	Pro	Ala Thr Thr
2690		2695		2700	
Val Lys	Asp Lys Ala Lys	Ala	Asp Val Asn Ala	Glu	Lys Glu Glu
2705		2710		2715	
Lys Asn	Leu Gln Ile Asn	Ser	Asn Asp Glu Ala	Thr	Thr Glu Glu
2720		2725		2730	
Lys Leu	Val Ala Ser Asp	Asn	Leu Asn His Val	Val	Glu Thr Thr
2735		2740		2745	
Asn Gln	Ala Ile Glu Asp	Ala	Pro Asp Thr Asn	Gln	Val Asn Val
2750		2755		2760	
Glu Lys	Asn Lys Gly Ile	Gly	Thr Ile Arg Asp	Ile	Gln Pro Leu
2765		2770		2775	
Val Val	Lys Lys Pro Thr	Ala	Lys Ser Lys Ile	Glu	Ser Ala Val
2780		2785		2790	
Glu Lys	Lys Lys Thr Glu	Ile	Asn Gln Thr Gln	Asn	Ala Thr His
2795		2800		2805	
Asp Glu	Val Arg Glu Gly	Leu	Asn Gln Leu Asn	Gln	Ile His Glu
2810		2815		2820	
Lys Ala	Lys Asn Asp Val	Asn	Gln Ser Gln Thr	Asn	Gln Gln Val
2825		2830		2835	
Glu Asn	Ala Glu Gln Asn	Ser	Leu Asp Gln Ile	Asn	Asn Phe Arg
2840		2845		2850	
Pro Asp	Phe Ser Lys Lys	Arg	Asn Ala Val Ala	Glu	Ile Val Lys

2855		2860		2865
Ala Gln Gln Asn Lys Ile Asp	Glu Ile Glu Gln Glu Phe Ser Ala			
2870	2875	2880		
Thr Gln Glu Glu Lys Asp Asn	Ala Leu Gln His Leu Asp Glu Gln			
2885	2890	2895		
Val Lys Glu Ile Ile Asn Ser	Ile Asn Gln Ala Asn Thr Asp Asn			
2900	2905	2910		
Glu Val Asp Asn Ala Lys Thr	Ser Gly Leu Asn Asn Ile Thr Glu			
2915	2920	2925		
Tyr Arg Pro Glu Tyr Asn Lys	Lys Lys Asn Ala Ile Leu Lys Leu			
2930	2935	2940		
Tyr Asp Val Ser Asp Thr Gln	Glu Ala Ile Ile Asn Gly Tyr Pro			
2945	2950	2955		
Asp Ala Thr Glu Asp Glu Leu	Gln Glu Ala Asn Ser Lys Leu Asn			
2960	2965	2970		
Lys Ile Leu Leu Asp Ala Lys	Lys Gln Ile Gly Leu Ala His Thr			
2975	2980	2985		
Asn Asn Glu Val Asp Asp Ile	Tyr Asn Glu Val Ser Gln Lys Met			
2990	2995	3000		
Lys Thr Ile Leu Pro Arg Val	Asp Thr Lys Ala Val Ala Arg Ser			
3005	3010	3015		
Val Leu Asn Ala Leu Ala Lys	Gln Leu Ile Lys Thr Phe Glu Asn			
3020	3025	3030		
Thr Ala Asp Val Thr His Glu	Glu Arg Asn Asp Ala Ile Asn His			
3035	3040	3045		
Val Lys Glu Gln Leu Ser Leu	Val Phe Asn Ala Ile Glu Lys Asp			
3050	3055	3060		
Arg Lys Asp Ile Gln Val Ala	Gln Asp Glu Leu Phe Gly Leu Asn			
3065	3070	3075		
Glu Leu Asn Ser Ile Phe Ile	Asn Ile Thr Gln Lys Pro Thr Ala			
3080	3085	3090		

Arg	Lys	Ala	Ile	Ser	Gly	Met	Ala	Ser	Gln	Leu	Asn	Asn	Ser	Ile
3095						3100					3105			
Asn	Asn	Thr	Pro	Tyr	Ala	Thr	Glu	Glu	Glu	Arg	Gln	Ile	Ala	Leu
3110						3115					3120			
Asn	Lys	Val	Lys	Ala	Ile	Val	Asp	Asp	Ala	Asn	Glu	Lys	Ile	Arg
3125						3130					3135			
Glu	Ala	Asn	Thr	Asp	Ser	Glu	Val	Leu	Gly	Thr	Lys	Ser	Asn	Ala
3140						3145					3150			
Ile	Thr	Leu	Leu	Gln	Ala	Ile	Ser	Ala	Asp	Val	Gln	Val	Lys	Pro
3155						3160					3165			
Gln	Ala	Phe	Glu	Glu	Ile	Asn	Ala	Gln	Ala	Glu	Ile	Gln	Arg	Glu
3170						3175					3180			
Arg	Ile	Asn	Gly	Asn	Ser	Asp	Ala	Thr	Arg	Glu	Glu	Lys	Glu	Glu
3185						3190					3195			
Ala	Leu	Lys	Gln	Val	Asp	Thr	Leu	Val	Asn	His	Ser	Phe	Ile	Thr
3200						3205					3210			
Ile	Asn	Asn	Val	Asn	Lys	Asn	Gln	Glu	Val	Tyr	Asp	Thr	Lys	Asp
3215						3220					3225			
Lys	Thr	Ile	Glu	Ala	Ile	His	Lys	Ile	Lys	Pro	Ile	Ser	Thr	Ile
3230						3235					3240			
Lys	Pro	Gln	Ala	Leu	Asn	Glu	Ile	Thr	Ile	Gln	Leu	Asp	Thr	Gln
3245						3250					3255			
Arg	Asp	Leu	Ile	Lys	Asn	Asn	Lys	Glu	Ser	Thr	Val	Glu	Glu	Lys
3260						3265					3270			
Ala	Ser	Ala	Ile	Asp	Lys	Leu	Ile	Lys	Thr	Ala	Ala	Arg	Ile	Ala
3275						3280					3285			
Glu	Ser	Ile	Asp	Lys	Ala	Gln	Thr	Asn	Glu	Glu	Val	Lys	Asn	Ile
3290						3295					3300			
Lys	Lys	Gln	Ser	Ile	Asp	Glu	Ile	Ser	Lys	Ile	Leu	Pro	Val	Ile
3305						3310					3315			

Glu	Ile	Lys	Ser	Ala	Ala	Arg	Asn	Glu	Ile	His	Gln	Lys	Ala	Glu
3320						3325					3330			
Val	Ile	Arg	Gly	Leu	Ile	Asn	Asp	Asn	Glu	Glu	Ala	Thr	Lys	Glu
3335						3340					3345			
Glu	Lys	Asp	Ile	Ala	Leu	Asn	Gln	Leu	Asp	Thr	Thr	Leu	Thr	Gln
3350						3355					3360			
Ala	Asn	Val	Ser	Ile	Asp	Gln	Ala	Leu	Thr	Asn	Glu	Ala	Val	Asn
3365						3370					3375			
Arg	Ala	Lys	Glu	Ile	Ala	Asn	Ser	Glu	Ile	Asn	Lys	Ile	Ser	Val
3380						3385					3390			
Ile	Ala	Ile	Lys	Lys	Pro	Glu	Ala	Ile	Ala	Glu	Ile	Gln	Glu	Leu
3395						3400					3405			
Ala	Asp	Lys	Lys	Leu	Asn	Lys	Phe	Lys	Gln	Ser	Gln	Glu	Ala	Thr
3410						3415					3420			
Ile	Glu	Glu	Lys	Gln	Ser	Ala	Ile	Asn	Glu	Leu	Glu	Gln	Ala	Leu
3425						3430					3435			
Lys	Ser	Ala	Ile	Asn	His	Ile	His	Gln	Ser	Gln	Asn	Asn	Glu	Ser
3440						3445					3450			
Val	Ser	Ala	Ala	Leu	Lys	Glu	Ser	Ile	Ser	Leu	Ile	Asp	Ser	Ile
3455						3460					3465			
Glu	Ile	Gln	Ala	His	Lys	Lys	Leu	Glu	Ala	Lys	Ala	Tyr	Ile	Asp
3470						3475					3480			
Gly	Tyr	Ser	Asp	Asp	Lys	Ile	Asn	Asp	Ile	Ser	Ser	Arg	Ala	Thr
3485						3490					3495			
Asn	Glu	Glu	Lys	Gln	Ile	Phe	Val	Ser	Lys	Leu	Lys	Ala	Leu	Ile
3500						3505					3510			
Asn	Arg	Thr	His	Lys	Gln	Ile	Asp	Glu	Ala	Glu	Thr	Phe	Val	Ser
3515						3520					3525			
Val	Glu	Thr	Ile	Val	Arg	Asn	Phe	Lys	Val	Glu	Ala	Asp	Lys	Leu
3530						3535					3540			

Asn Ser Ile Val Arg Lys Lys Ala Lys Ala Ser Lys Glu Ile Glu
3545 3550 3555

Leu Glu Ala Asp His Val Lys Gln Met Ile Asn Ala Asn Leu Ser
3560 3565 3570

Ala Ser Thr Arg Val Lys Gln Asn Ala Arg Thr Leu Ile Asn Glu
3575 3580 3585

Ile Val Ser Asn Ala Leu Ser Gln Leu Asn Lys Val Thr Thr Asn
3590 3595 3600

Lys Glu Val Asp Glu Ile Val Asn Glu Thr Ile Glu Lys Leu Lys
3605 3610 3615

Ser Ile Gln Ile Arg Glu Asp Lys Ile Leu Ser Ser Gln Arg Ser
3620 3625 3630

Ser Thr Ser Met Thr Glu Lys Ser Asn Gln Cys Tyr Ser Ser Glu
3635 3640 3645

Asn Asn Thr Ile Lys Ser Leu Pro Glu Ala Gly Asn Ala Asp Lys
3650 3655 3660

Ser Leu Pro Leu Ala Gly Val Thr Leu Ile Ser Gly Leu Ala Ile
3665 3670 3675

Met Ser Ser Arg Lys Lys Lys Lys Asp Lys Lys Val Asn Asp
3680 3685 3690

<210> 49

<211> 439

<212> PRT

<213> Staphylococcus epidermidis

<400> 49

Leu Asp Ile Lys Met Pro Lys Leu Gly Glu Ser Val His Glu Gly Thr
1 5 10 15

Ile Glu Gln Trp Leu Val Ser Val Gly Asp His Val Asp Glu Tyr Glu
20 25 30

Pro Leu Cys Glu Val Ile Thr Asp Lys Val Thr Ala Glu Val Pro Ser
35 40 45

Thr Ile Ser Gly Thr Ile Thr Glu Leu Val Val Glu Glu Gly Gln Thr
50 55 60

Val Asn Ile Asn Thr Val Ile Cys Lys Ile Asp Ser Glu Asn Gly Gln
65 70 75 80

Asn Gln Thr Glu Ser Ala Asn Glu Phe Lys Glu Glu Gln Asn Gln His
85 90 95

Ser Gln Ser Asn Ile Asn Val Ser Gln Phe Glu Asn Asn Pro Lys Thr
100 105 110

His Glu Ser Glu Val His Thr Ala Ser Ser Arg Ala Asn Asn Asn Gly
115 120 125

Arg Phe Ser Pro Val Val Phe Lys Leu Ala Ser Glu His Asp Ile Asp
130 135 140

Leu Thr Gln Val Lys Gly Thr Gly Phe Glu Gly Arg Val Thr Lys Lys
145 150 155 160

Asp Ile Gln Asn Ile Ile Asn Asn Pro Asn Asp Gln Glu Lys Glu Lys
165 170 175

Glu Phe Lys Gln Thr Asp Lys Lys Asp His Ser Thr Asn His Cys Asp
180 185 190

Phe Leu His Gln Ser Ser Thr Lys Asn Glu His Ser Pro Leu Ser Asn
195 200 205

Glu Arg Val Val Pro Val Lys Gly Ile Arg Lys Ala Ile Ala Gln Asn
210 215 220

Met Val Thr Ser Val Ser Glu Ile Pro His Gly Trp Met Met Val Glu
225 230 235 240

Ala Asp Ala Thr Asn Leu Val Gln Thr Arg Asn Tyr His Lys Ala Gln
245 250 255

Phe Lys Gln Asn Glu Gly Tyr Asn Leu Thr Phe Phe Ala Phe Phe Val
260 265 270

Lys Ala Val Ala Glu Ala Leu Lys Val Asn Pro Leu Leu Asn Ser Thr
275 280 285

Trp Gln Gly Asp Glu Ile Val Ile His Lys Asp Ile Asn Ile Ser Ile
290 295 300

Ala Val Ala Asp Asp Asp Lys Leu Tyr Val Pro Val Ile Lys Asn Ala
305 310 315 320

Asp Glu Lys Ser Ile Lys Gly Ile Ala Arg Glu Ile Asn Asp Leu Ala
325 330 335

Thr Lys Ala Arg Leu Gly Lys Leu Ala Gln Ser Asp Met Gln Asn Gly
340 345 350

Thr Phe Thr Val Asn Asn Thr Gly Ser Phe Gly Ser Val Ser Ser Met
355 360 365

Gly Ile Ile Asn His Pro Gln Ala Ala Ile Leu Gln Val Glu Ser Val
370 375 380

Val Lys Lys Pro Val Val Ile Asp Asp Met Ile Ala Ile Arg Asn Met
385 390 395 400

Val Asn Leu Cys Ile Ser Ile Asp His Arg Ile Leu Asp Gly Val Gln
405 410 415

Thr Gly Lys Phe Met Asn Leu Val Lys Lys Lys Ile Glu Gln Tyr Ser
420 425 430

Ile Glu Asn Thr Ser Ile Tyr
435

<210> 50
<211> 295
<212> PRT
<213> Staphylococcus epidermidis

<400> 50

Met Asn Thr Ile Ile Glu Glu Tyr Leu Asn Phe Ile Gln Ile Glu Lys
1 5 10 15

Gly Leu Ser Asn Asn Thr Ile Gly Ala Tyr Arg Arg Asp Leu Lys Lys
20 25 30

Tyr Lys Asp Tyr Leu Glu Asp Asn Lys Ile Ser His Ile Asp Phe Ile
35 40 45

Asp Arg Gln Ile Ile Gln Glu Cys Leu Gly His Leu Ile Asp Met Gly
50 55 60

Gln Ser Ser Lys Ser Leu Ala Arg Phe Ile Ser Thr Ile Arg Ser Phe

65	70	75	80
His Gln Phe Ala Leu Arg Glu Lys Tyr Ala Ala Lys Asp Pro Thr Val	85	90	95
Leu Ile Glu Thr Pro Lys Tyr Glu Lys Lys Leu Pro Asp Val Leu Glu	100	105	110
Ile Asp Glu Val Ile Ala Leu Leu Glu Thr Pro Asp Leu Thr Lys Asn	115	120	125
Asn Gly Tyr Arg Asp Arg Thr Met Leu Glu Leu Leu Tyr Ala Thr Gly	130	135	140
Met Arg Val Thr Glu Ile Ile Gln Leu Asp Val Glu Asp Val Asn Leu	145	150	155
Met Met Gly Phe Val Arg Val Phe Gly Lys Gly Asn Lys Glu Arg Ile	165	170	175
Val Pro Leu Gly Asp Thr Val Ile Glu Tyr Leu Thr Thr Tyr Ile Glu	180	185	190
Thr Val Arg Pro Gln Leu Leu Lys Gln Thr Thr Thr Gln Ala Leu Phe	195	200	205
Leu Asn Met His Gly Lys Ser Leu Ser Arg Gln Gly Ile Trp Lys Ile	210	215	220
Ile Lys Gln Tyr Gly Leu Lys Ala Asn Ile Asn Lys Thr Leu Thr Pro	225	230	235
His Thr Leu Arg His Ser Phe Ala Thr His Leu Leu Glu Asn Gly Ala	245	250	255
Asp Leu Arg Ala Val Gln Glu Met Leu Gly His Ser Asp Ile Ser Thr	260	265	270
Thr Gln Leu Tyr Thr His Val Ser Lys Ser Gln Ile Arg Lys Met Tyr	275	280	285
Thr Gln Phe His Pro Arg Ala	290	295	

<210> 51
 <211> 800

<212> PRT

<213> Staphylococcus epidermidis

<400> 51

Met Ser Leu Val Tyr Leu Met Ala Thr Asn Leu Leu Val Met Leu Ile
1 5 10 15

Val Leu Phe Thr Leu Ser His Arg Gln Leu Arg Lys Val Ala Gly Tyr
20 25 30

Val Ala Leu Ile Ala Pro Ile Val Thr Ser Thr Tyr Phe Ile Met Lys
35 40 45

Ile Pro Asp Val Ile Arg Asn Lys Phe Ile Ala Val Arg Leu Pro Trp
50 55 60

Met Pro Ser Ile Asp Ile Asn Leu Asp Leu Arg Leu Asp Gly Leu Ser
65 70 75 80

Leu Met Phe Gly Leu Ile Ile Ser Leu Ile Gly Val Gly Val Phe Phe
85 90 95

Tyr Ala Thr Gln Tyr Leu Ser His Ser Thr Asp Asn Leu Pro Arg Phe
100 105 110

Phe Ile Tyr Leu Leu Leu Phe Met Phe Ser Met Ile Gly Ile Val Ile
115 120 125

Ala Asn Asn Thr Ile Leu Met Tyr Val Phe Trp Glu Leu Thr Ser Ile
130 135 140

Ser Ser Phe Leu Leu Ile Ser Tyr Trp Tyr Asn Asn Gly Glu Ser Gln
145 150 155 160

Leu Gly Ala Ile Gln Ser Phe Met Ile Thr Val Phe Gly Gly Leu Ala
165 170 175

Leu Leu Thr Gly Phe Ile Ile Leu Tyr Ile Ile Thr Gly Thr Asn Thr
180 185 190

Ile Thr Asp Ile Leu Asn Gln Arg Asn Ala Ile Ser Arg His Pro Leu
195 200 205

Phe Ile Pro Met Ile Leu Met Leu Leu Leu Gly Ala Phe Thr Lys Ser
210 215 220

Ala Gln Phe Pro Phe His Ile Trp Leu Pro Lys Ala Met Ala Ala Pro
225 230 235 240

Thr Pro Val Ser Ala Tyr Leu His Ser Ala Thr Met Val Lys Ala Gly
245 250 255

Ile Phe Leu Leu Phe Arg Phe Thr Pro Leu Leu Gly Leu Ser Asn Val
260 265 270

Tyr Ile Tyr Thr Val Thr Phe Val Gly Leu Ile Thr Met Leu Phe Gly
275 280 285

Ser Leu Thr Ala Leu Arg Gln Tyr Asp Leu Lys Gly Ile Leu Ala Tyr
290 295 300

Ser Thr Ile Ser Gln Leu Gly Met Ile Met Thr Met Val Gly Leu Gly
305 310 315 320

Gly Gly Tyr Ala Gln His Thr Ser Asp Glu Leu Ser Lys Phe Tyr Ile
325 330 335

Leu Val Leu Phe Ala Gly Leu Phe His Leu Met Asn His Ala Val Phe
340 345 350

Lys Cys Ala Leu Phe Met Gly Val Gly Ile Ile Asp His Glu Ser Gly
355 360 365

Thr Arg Asp Ile Arg Leu Leu Asn Gly Met Arg Lys Val Phe Pro Lys
370 375 380

Met His Ile Val Met Leu Leu Ala Ala Leu Ser Met Ala Gly Val Pro
385 390 395 400

Phe Leu Asn Gly Phe Leu Ser Lys Glu Met Phe Leu Asp Ser Leu Thr
405 410 415

Lys Ala Asn Glu Leu Asp Gln Tyr Gly Phe Val Leu Thr Phe Val Ile
420 425 430

Ile Ser Ile Gly Val Ile Ala Ser Ile Leu Thr Phe Thr Tyr Ala Leu
435 440 445

Tyr Met Ile Lys Glu Thr Phe Trp Gly Asn Tyr Asn Ile Glu Lys Phe
450 455 460

Lys Arg Lys Gln Ile His Glu Pro Trp Leu Phe Ser Leu Pro Ala Val

465	470	475	480
Ile Leu Met Leu Leu Ile Pro Val Ile Phe Phe Val Pro Asn Val Phe	485	490	495
Gly Asn Phe Val Ile Leu Pro Ala Thr Arg Ser Val Ser Gly Ile Gly	500	505	510
Ala Glu Val Asp Ala Phe Val Pro His Ile Ser Gln Trp His Gly Val	515	520	525
Asn Leu Pro Leu Ile Leu Ser Ile Val Val Ile Ile Ile Gly Leu Ile	530	535	540
Leu Ala Leu Val Val Asn Trp Lys Glu Val Thr His Gln Ile Ile Lys	545	550	555
Ser Ala Ser Ile Thr Asp Gly Tyr Arg Lys Ile Tyr Arg Glu Phe Glu	565	570	575
Leu Tyr Ser Ala Arg Gly Ile Arg Ala Leu Met Asn Asn Lys Leu Asn	580	585	590
Tyr Tyr Ile Met Ile Thr Leu Phe Ile Phe Val Ala Ile Val Val Tyr	595	600	605
Gly Tyr Leu Thr Val Gly Phe Pro His Val His Gln Leu His Ile Ser	610	615	620
Ser Phe Gly Pro Leu Glu Val Ile Leu Ser Val Val Thr Leu Ile Ile	625	630	635
Gly Ile Ser Leu Ile Phe Ile Arg Gln Arg Leu Thr Met Val Val Leu	645	650	655
Asn Gly Met Ile Gly Phe Ala Val Thr Leu Tyr Phe Ile Ala Met Lys	660	665	670
Ala Pro Asp Leu Ala Leu Thr Gln Leu Val Val Glu Thr Ile Thr Thr	675	680	685
Ile Leu Phe Ile Val Ser Phe Ser Arg Leu Pro Asn Ile Pro Arg Val	690	695	700
Lys Ala Asn Leu Lys Lys Glu Thr Phe Lys Ile Ile Val Ser Leu Val	705	710	715
			720

Met Ala Leu Thr Val Val Ser Leu Ile Phe Val Ala Gln Gln Ala Asp
725 730 735

Gly Met Pro Ser Ile Ala Lys Phe Tyr Glu Asp Ala Tyr Glu Leu Thr
740 745 750

Gly Gly Lys Asn Ile Val Asn Ala Ile Leu Gly Asp Phe Arg Ala Leu
755 760 765

Asp Thr Met Phe Glu Gly Leu Val Leu Ile Ile Ala Gly Leu Gly Ile
770 775 780

Tyr Thr Leu Leu Asn Tyr Lys Asp Arg Arg Gly Gln Asp Glu Arg Glu
785 790 795 800

<210> 52

<211> 892

<212> PRT

<213> Staphylococcus epidermidis

<400> 52

Leu Phe Gly Leu Gly His Asn Glu Ala Lys Ala Glu Glu Asn Thr Val
1 5 10 15

Gln Asp Val Lys Asp Ser Asn Met Asp Asp Glu Leu Ser Asp Ser Asn
20 25 30

Asp Gln Ser Ser Asn Glu Glu Lys Asn Asp Val Ile Asn Asn Ser Gln
35 40 45

Ser Ile Asn Thr Asp Asp Asp Asn Gln Ile Lys Lys Glu Glu Thr Asn
50 55 60

Ser Asn Asp Ala Ile Glu Asn Arg Ser Lys Asp Ile Thr Gln Ser Thr
65 70 75 80

Thr Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr Pro Gln
85 90 95

Asp Asn Thr Gln Leu Lys Glu Glu Val Val Lys Glu Pro Ser Ser Val
100 105 110

Glu Ser Ser Asn Ser Ser Met Asp Thr Ala Gln Gln Pro Ser His Thr
115 120 125

Thr Ile Asn Ser Glu Ala Ser Ile Gln Thr Ser Asp Asn Glu Glu Asn
130 135 140

Ser Arg Val Ser Asp Phe Ala Asn Ser Lys Ile Ile Glu Ser Asn Thr
145 150 155 160

Glu Ser Asn Lys Glu Glu Asn Thr Ile Glu Gln Pro Asn Lys Val Arg
165 170 175

Glu Asp Ser Ile Thr Ser Gln Pro Ser Ser Tyr Lys Asn Ile Asp Glu
180 185 190

Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn Leu Pro Ile Asn Glu Tyr
195 200 205

Glu Asn Lys Val Arg Pro Leu Ser Thr Thr Ser Ala Gln Pro Ser Ser
210 215 220

Lys Arg Val Thr Val Asn Gln Leu Ala Ala Glu Gln Gly Ser Asn Val
225 230 235 240

Asn His Leu Ile Lys Val Thr Asp Gln Ser Ile Thr Glu Gly Tyr Asp
245 250 255

Asp Ser Asp Gly Ile Ile Lys Ala His Asp Ala Glu Asn Leu Ile Tyr
260 265 270

Asp Val Thr Phe Glu Val Asp Asp Lys Val Lys Ser Gly Asp Thr Met
275 280 285

Thr Val Asn Ile Asp Lys Asn Thr Val Pro Ser Asp Leu Thr Asp Ser
290 295 300

Phe Ala Ile Pro Lys Ile Lys Asp Asn Ser Gly Glu Ile Ile Ala Thr
305 310 315 320

Gly Thr Tyr Asp Asn Thr Asn Lys Gln Ile Thr Tyr Thr Phe Thr Asp
325 330 335

Tyr Val Asp Lys Tyr Glu Asn Ile Lys Ala His Leu Lys Leu Thr Ser
340 345 350

Tyr Ile Asp Lys Ser Lys Val Pro Asn Asn Asn Thr Lys Leu Asp Val
355 360 365

Glu Tyr Lys Thr Ala Leu Ser Ser Val Asn Lys Thr Ile Thr Val Glu

370		375		380
Tyr Gln Lys Pro Asn Glu Asn Arg Thr Ala Asn Leu Gln Ser Met Phe				
385		390		395 400
Thr Asn Ile Asp Thr Lys Asn His Thr Val Glu Gln Thr Ile Tyr Ile				
	405		410	415
Asn Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile Ser Gly				
	420		425	430
Asn Gly Asp Glu Gly Ser Thr Ile Ile Asp Asp Ser Thr Ile Ile Lys				
	435		440	445
Val Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn Arg Ile				
	450		455	460
Tyr Asp Tyr Ser Glu Tyr Glu Asp Val Thr Asn Asp Asp Tyr Ala Gln				
465		470		475 480
Leu Gly Asn Asn Asn Asp Val Asn Ile Asn Phe Gly Asn Ile Asp Ser				
	485		490	495
Pro Tyr Ile Ile Lys Val Ile Ser Lys Tyr Asp Pro Asn Lys Asp Asp				
	500		505	510
Tyr Thr Thr Ile Gln Gln Thr Val Thr Met Gln Thr Thr Ile Asn Glu				
	515		520	525
Tyr Thr Gly Glu Phe Arg Thr Ala Ser Tyr Asp Asn Thr Ile Ala Phe				
	530		535	540
Ser Thr Ser Ser Gly Gln Gly Gln Gly Asp Leu Pro Pro Glu Lys Thr				
545		550		555 560
Tyr Lys Ile Gly Asp Tyr Val Trp Glu Asp Val Asp Lys Asp Gly Ile				
	565		570	575
Gln Asn Thr Asn Asp Asn Glu Lys Pro Leu Ser Asn Val Leu Val Thr				
	580		585	590
Leu Thr Tyr Pro Asp Gly Thr Ser Lys Ser Val Arg Thr Asp Glu Glu				
	595		600	605
Gly Lys Tyr Gln Phe Asp Gly Leu Lys Asn Gly Leu Thr Tyr Lys Ile				
610		615		620

Thr Phe Glu Thr Pro Glu Gly Tyr Thr Pro Thr Leu Lys His Ser Gly
625 630 635 640

Thr Asn Pro Ala Leu Asp Ser Glu Gly Asn Ser Val Trp Val Thr Ile
645 650 655

Asn Gly Gln Asp Asp Met Thr Ile Asp Ser Gly Phe Tyr Gln Thr Pro
660 665 670

Lys Tyr Ser Leu Gly Asn Tyr Val Trp Tyr Asp Thr Asn Lys Asp Gly
675 680 685

Ile Gln Gly Asp Asp Glu Lys Gly Ile Ser Gly Val Lys Val Thr Leu
690 695 700

Lys Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Thr Thr Asp Glu Asn
705 710 715 720

Gly Lys Tyr Gln Phe Asp Asn Leu Asn Ser Gly Asn Tyr Ile Val His
725 730 735

Phe Asp Lys Pro Ser Gly Met Thr Gln Thr Thr Thr Asp Ser Gly Asp
740 745 750

Asp Asp Glu Gln Asp Ala Asp Gly Glu Glu Val His Val Thr Ile Thr
755 760 765

Asp His Asp Asp Phe Ser Ile Asp Asn Gly Tyr Tyr Asp Asp Asp Ser
770 775 780

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
785 790 795 800

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
805 810 815

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
820 825 830

Ser Asp Ser Asp Ser Asp Ser Gly Leu Asp Asn Ser Ser Asp Lys Asn
835 840 845

Thr Lys Asp Lys Leu Pro Asp Thr Gly Ala Asn Glu Asp His Asp Ser
850 855 860

Lys Gly Thr Leu Leu Gly Ala Leu Phe Ala Gly Leu Gly Ala Leu Leu
865 870 875 880

Leu Gly Lys Arg Arg Lys Asn Arg Lys Asn Lys Asn
885 890

<210> 53
<211> 484
<212> PRT
<213> Staphylococcus epidermidis

<400> 53

Met Ser Glu Arg Ile Arg Val Arg Tyr Ala Pro Ser Pro Thr Gly Tyr
1 5 10 15

Leu His Ile Gly Asn Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala
20 25 30

Lys His Tyr Asn Gly Asp Phe Val Val Arg Ile Glu Asp Thr Asp Ser
35 40 45

Lys Arg Asn Leu Glu Asp Gly Glu Ser Ser Gln Phe Asp Asn Leu Lys
50 55 60

Trp Leu Gly Leu Asp Trp Asp Glu Ser Val Asp Lys Asp Lys Gly Phe
65 70 75 80

Gly Pro Tyr Arg Gln Ser Glu Arg Ala Glu Ile Tyr Asn Pro Leu Ile
85 90 95

Gln Gln Leu Leu Glu Glu Asp Lys Ala Tyr Lys Cys Tyr Met Thr Glu
100 105 110

Glu Glu Leu Glu Ala Glu Arg Glu Ala Gln Ile Ala Arg Gly Glu Met
115 120 125

Pro Arg Tyr Gly Gly Gln His Ala His Leu Thr Glu Glu Gln Arg Gln
130 135 140

Gln Tyr Glu Ala Glu Gly Arg Lys Pro Ser Ile Arg Phe Arg Val Pro
145 150 155 160

Lys Asp Gln Thr Tyr Thr Phe Asn Asp Met Val Lys Gly Glu Ile Ser
165 170 175

Phe Glu Ser Asp Asn Ile Gly Asp Trp Val Ile Val Lys Lys Asp Gly

180								185				190				
Val	Pro	Thr	Tyr	Asn	Phe	Ala	Val	Ala	Val	Asp	Asp	His	Tyr	Met	Gln	
	195						200					205				
Ile	Ser	Asp	Val	Ile	Arg	Gly	Asp	Asp	His	Val	Ser	Asn	Thr	Pro	Lys	
	210					215					220					
Gln	Leu	Met	Ile	Tyr	Glu	Ala	Phe	Gly	Trp	Glu	Ala	Pro	Arg	Phe	Gly	
225					230					235					240	
His	Met	Ser	Leu	Ile	Val	Asn	Glu	Glu	Arg	Lys	Lys	Leu	Ser	Lys	Arg	
			245						250					255		
Asp	Gly	Gln	Ile	Leu	Gln	Phe	Ile	Glu	Gln	Tyr	Arg	Asp	Leu	Gly	Tyr	
			260						265				270			
Leu	Pro	Glu	Ala	Leu	Phe	Asn	Phe	Ile	Thr	Leu	Leu	Gly	Trp	Ser	Pro	
		275					280					285				
Glu	Gly	Glu	Glu	Glu	Ile	Phe	Ser	Lys	Glu	Glu	Phe	Ile	Lys	Ile	Phe	
	290					295					300					
Asp	Glu	Lys	Arg	Leu	Ser	Lys	Ser	Pro	Ala	Met	Phe	Asp	Arg	Gln	Lys	
305					310					315					320	
Leu	Ala	Trp	Val	Asn	Asn	Gln	Tyr	Met	Lys	Thr	Lys	Asp	Thr	Glu	Thr	
				325					330					335		
Val	Phe	Glu	Leu	Ala	Leu	Pro	His	Leu	Ile	Lys	Ala	Asn	Leu	Ile	Pro	
			340						345				350			
Glu	Asn	Pro	Ser	Glu	Lys	Asp	Arg	Glu	Trp	Gly	Arg	Lys	Leu	Ile	Ala	
		355					360					365				
Leu	Tyr	Gln	Lys	Glu	Met	Ser	Tyr	Ala	Gly	Glu	Ile	Val	Pro	Leu	Ser	
	370					375					380					
Glu	Met	Phe	Phe	His	Glu	Met	Pro	Glu	Leu	Gly	Lys	Asp	Glu	Gln	Glu	
385					390					395					400	
Val	Leu	Gln	Gly	Glu	Gln	Val	Pro	Glu	Leu	Met	Asn	His	Leu	Tyr	Gly	
				405					410					415		
Lys	Leu	Glu	Ser	Leu	Glu	Ser	Phe	Glu	Ala	Thr	Glu	Ile	Lys	Lys	Met	
			420						425				430			

Ile Lys Glu Val Gln Lys Glu Thr Gly Ile Lys Gly Lys Gln Leu Phe
435 440 445

Met Pro Ile Arg Val Ala Val Thr Gly Gln Met His Gly Pro Glu Leu
450 455 460

Pro Asn Thr Ile Glu Val Leu Gly Lys Asp Lys Val Leu Ser Arg Leu
465 470 475 480

Lys Asn Leu Val

<210> 54

<211> 296

<212> PRT

<213> Staphylococcus epidermidis

<400> 54

Met Glu Tyr Lys Asp Ile Ala Thr Pro Ser Arg Thr Arg Ala Leu Leu
1 5 10 15

Asp Gln Tyr Gly Phe Asn Phe Lys Lys Ser Leu Gly Gln Asn Phe Leu
20 25 30

Ile Asp Val Asn Ile Ile Asn Lys Ile Ile Glu Ala Ser His Ile Asp
35 40 45

Cys Thr Thr Gly Val Ile Glu Val Gly Pro Gly Met Gly Ser Leu Thr
50 55 60

Glu Gln Leu Ala Lys Asn Ala Lys Lys Val Met Ala Phe Glu Ile Asp
65 70 75 80

Gln Arg Leu Ile Pro Val Leu Lys Asp Thr Leu Ser Pro Tyr Asp Asn
85 90 95

Val Thr Ile Ile Asn Glu Asp Ile Leu Lys Ala Asp Ile Ala Lys Ala
100 105 110

Val Asp Thr His Leu Gln Asp Cys Asp Lys Ile Met Val Val Ala Asn
115 120 125

Leu Pro Tyr Tyr Ile Thr Thr Pro Ile Leu Leu Asn Leu Met Gln Gln
130 135 140

Asp Val Pro Ile Asp Gly Phe Val Val Met Met Gln Lys Glu Val Gly
145 150 155 160

Glu Arg Leu Asn Ala Gln Val Gly Thr Lys Ala Tyr Gly Ser Leu Ser
165 170 175

Ile Val Ala Gln Tyr Tyr Thr Glu Thr Ser Lys Val Leu Thr Val Pro
180 185 190

Lys Thr Val Phe Met Pro Pro Pro Asn Val Asp Ser Ile Val Val Lys
195 200 205

Leu Met Gln Arg Gln Glu Pro Leu Val Gln Val Asp Asp Glu Glu Gly
210 215 220

Phe Phe Lys Leu Ala Lys Ala Ala Phe Ala Gln Arg Arg Lys Thr Ile
225 230 235 240

Asn Asn Asn Tyr Gln Asn Phe Phe Lys Asp Gly Lys Lys Asn Lys Glu
245 250 255

Thr Ile Arg Gln Trp Leu Glu Ser Ala Gly Ile Asp Pro Lys Arg Arg
260 265 270

Gly Glu Thr Leu Thr Ile Gln Asp Phe Ala Thr Leu Tyr Glu Gln Lys
275 280 285

Lys Lys Phe Ser Glu Leu Thr Asn
290 295

<210> 55
<211> 106
<212> PRT
<213> Staphylococcus epidermidis

<400> 55

Met Thr Ser Asn His His Ala Pro Tyr Asp Leu Gly Tyr Thr Arg Ala
1 5 10 15

Thr Met Asp Asn Thr Lys Gly Ser Glu Thr Ala Arg Ser Ser Lys Ser
20 25 30

His Lys Val Val Leu Ser Ser Asp Cys Ser Leu Gln Leu Asp Tyr Met
35 40 45

Lys Leu Glu Ser Leu Val Ile Val Asp Gln His Ala Thr Val Asn Thr
50 55 60

Phe Pro Gly Leu Val His Thr Ala Arg His Thr Thr Arg Val Cys Asn
65 70 75 80

Thr Arg Ser Arg Trp Ser Asn His Leu Glu Leu Ala Val Glu Gly Gly
85 90 95

Thr Asn Asp Trp Gly Glu Val Val Thr Arg
100 105

<210> 56
<211> 442
<212> PRT
<213> Staphylococcus epidermidis

<400> 56

Met Phe Phe Lys Gln Phe Tyr Asp Lys His Leu Ser Gln Ala Ser Tyr
1 5 10 15

Leu Ile Gly Cys Gln Lys Thr Gly Glu Ala Met Ile Ile Asp Pro Ile
20 25 30

Arg Asp Leu Ser Ser Tyr Ile Arg Val Ala Asp Glu Glu Gly Leu Thr
35 40 45

Ile Thr His Ala Ala Glu Thr His Ile His Ala Asp Phe Ala Ser Gly
50 55 60

Ile Arg Asp Val Ala Ile Lys Leu Asn Ala Ser Ile Tyr Val Ser Gly
65 70 75 80

Glu Ser Asp Asp Thr Leu Gly Tyr Lys Asn Met Pro Asn Gln Thr His
85 90 95

Phe Val Gln His Asn Asp Asp Ile Tyr Val Gly Asn Ile Lys Leu Lys
100 105 110

Val Leu His Thr Pro Gly His Thr Pro Glu Ser Ile Ser Phe Leu Leu
115 120 125

Thr Asp Glu Gly Ala Gly Ala Gln Val Pro Met Gly Leu Phe Ser Gly
130 135 140

Asp Phe Ile Phe Val Gly Asp Ile Gly Arg Pro Asp Leu Leu Glu Lys
145 150 155 160

Ala Val Lys Val Glu Gly Ser Ser Glu Ile Gly Ala Lys Gln Met Phe
165 170 175

Lys Ser Ile Glu Ser Ile Lys Asp Leu Pro Asn Tyr Ile Gln Ile Trp
180 185 190

Pro Gly His Gly Ala Gly Ser Pro Cys Gly Lys Ser Leu Gly Ala Ile
195 200 205

Pro Thr Ser Thr Leu Gly Tyr Glu Lys Gln Thr Asn Trp Ala Phe Ser
210 215 220

Glu Asn Asn Glu Ala Thr Phe Ile Asp Lys Leu Ile Ser Asp Gln Pro
225 230 235 240

Ala Pro Pro His His Phe Ala Gln Met Lys Lys Ile Asn Gln Phe Gly
245 250 255

Met Asn Leu Tyr Gln Pro Tyr Thr Val Tyr Pro Ala Thr Asn Thr Asn
260 265 270

Arg Leu Thr Phe Asp Leu Arg Ser Lys Glu Ala Tyr His Gly Gly His
275 280 285

Ile Glu Gly Thr Ile Asn Ile Pro Tyr Asp Lys Asn Phe Ile Asn Gln
290 295 300

Ile Gly Trp Tyr Leu Asn Tyr Asp Gln Glu Ile Asn Leu Ile Gly Glu
305 310 315 320

Tyr His Leu Val Ser Lys Ala Thr His Thr Leu Gln Leu Ile Gly Tyr
325 330 335

Asp Asp Val Ala Gly Tyr Gln Leu Pro Gln Ser Lys Ile Gln Thr Arg
340 345 350

Ser Ile His Ser Glu Asp Ile Thr Gly Asn Glu Ser His Ile Leu Asp
355 360 365

Val Arg Asn Asp Asn Glu Trp Asn Asn Gly His Leu Ser Gln Ala Val
370 375 380

His Val Pro His Gly Lys Leu Leu Glu Thr Asp Leu Pro Phe Asn Arg
385 390 395 400

Asn Asp Val Ile Tyr Val His Cys Gln Ser Gly Ile Arg Ser Ser Ile

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405
Ala Ile Gly Ile Leu Glu His Lys Gly Tyr His Asn Ile Ile Asn Val
420 425 430
Asn Glu Gly Tyr Lys Asp Ile His Leu Ser
435 440
<210> 57
<211> 285
<212> PRT
<213> Staphylococcus epidermidis
<400> 57
Leu Lys Lys Ile Leu Val Leu Ser Leu Thr Ala Phe Leu Val Leu Ala
1 5 10 15
Gly Cys Asn Ser Gly Asp Lys Thr Asp Thr Lys Asp Lys Lys Glu Glu
20 25 30
Thr Lys Gln Thr Ser Lys Ala Asn Lys Glu Asn Lys Glu Gln His His
35 40 45
Lys Gln Glu Asn Asp Asn Lys Ala Ser Thr Gln Leu Ser Glu Lys Glu
50 55 60
Arg Leu Ala Leu Ala Phe Tyr Ala Asp Gly Val Glu Lys Tyr Met Leu
65 70 75 80
Thr Lys Asn Glu Val Leu Thr Gly Val Tyr Asp Tyr Gln Lys Gly Asn
85 90 95
Glu Thr Glu Lys Lys Gln Met Glu Gln Leu Met Leu Glu Lys Ala Asp
100 105 110
Ser Met Lys Asn Ala Pro Lys Asp Met Lys Phe Tyr Gln Val Tyr Pro
115 120 125
Ser Lys Gly Gln Phe Ala Ser Ile Val Gly Val Asn Lys Asn Lys Ile
130 135 140
Phe Ile Gly Ser Thr Gln Gly Ala Leu Ile Asp Tyr Gln Thr Leu Leu
145 150 155 160
Asn Asn Gly Lys Glu Leu Asp Ile Ser Gln Leu Tyr Glu Asp Asn Lys
165 170 175

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Asp Asn Arg Ser Leu Glu Glu Met Lys Asn Lys Ile Glu Ile Val Asp
180 185 190

Ser Gly Ala Ala Gln Lys Ala Asp Asp Pro Asp Lys Asn Ser Ala Asn
195 200 205

Thr Met Ala His Met Arg Ser Gln Ile Tyr Glu Lys Ile Ser Asp Phe
210 215 220

Asp Gly Lys Leu Asp Asn Lys Thr Tyr Leu Trp Asp Asn Ile Arg Ile
225 230 235 240

Asn Asp Asp Gly Asn Trp Thr Val His Tyr Arg Asn His Asp Gly Glu
245 250 255

Ile Met Gly Thr Tyr Lys Ser Glu Lys Asn Lys Ile Ile Lys Leu Asp
260 265 270

Gln Asn Gly Asn Lys Ile Lys Glu Gln Gln Met Ser Asn
275 280 285

<210> 58
<211> 498
<212> PRT
<213> Staphylococcus epidermidis

<400> 58

Met Ala Asn Lys Glu Ser Lys Asn Val Val Ile Ile Gly Ala Gly Val
1 5 10 15

Leu Ser Thr Thr Phe Gly Ser Met Ile Lys Glu Leu Glu Pro Asp Trp
20 25 30

Asn Ile Lys Leu Tyr Glu Arg Leu Asp Arg Pro Gly Ile Glu Ser Ser
35 40 45

Asn Glu Arg Asn Asn Ala Gly Thr Gly His Ala Ala Leu Cys Glu Leu
50 55 60

Asn Tyr Thr Val Gln Gln Pro Asp Gly Ser Ile Asp Ile Glu Lys Ala
65 70 75 80

Lys Glu Ile Asn Glu Gln Phe Glu Ile Ser Lys Gln Phe Trp Gly His
85 90 95

Leu Val Lys Ser Gly Asn Ile Ser Asn Pro Arg Asp Phe Ile Asn Pro

100							105					110				
Leu	Pro	His	Ile	Ser	Phe	Val	Arg	Gly	Lys	Asn	Asn	Val	Lys	Phe	Leu	
		115						120							125	
Lys	Asn	Arg	Tyr	Glu	Ala	Met	Arg	Asn	Phe	Pro	Met	Phe	Asp	Asn	Ile	
	130					135					140					
Glu	Tyr	Thr	Glu	Asp	Ile	Glu	Glu	Met	Arg	Lys	Trp	Met	Pro	Leu	Met	
145					150					155				160		
Met	Thr	Gly	Arg	Thr	Gly	Asn	Glu	Ile	Met	Ala	Ala	Ser	Lys	Ile	Asp	
				165					170					175		
Glu	Gly	Thr	Asp	Val	Asn	Tyr	Gly	Glu	Leu	Thr	Arg	Lys	Met	Ala	Lys	
			180					185						190		
Ser	Ile	Glu	Lys	His	Pro	Asn	Ala	Asp	Val	Gln	Tyr	Asn	His	Glu	Val	
		195				200						205				
Ile	Asn	Phe	Asn	Arg	Arg	Lys	Asp	Gly	Ile	Trp	Glu	Val	Lys	Val	Lys	
	210					215					220					
Asn	Arg	Asn	Ser	Gly	Asp	Val	Glu	Thr	Val	Leu	Ala	Asp	Tyr	Val	Phe	
225					230					235				240		
Ile	Gly	Ala	Gly	Gly	Gly	Ala	Ile	Pro	Leu	Leu	Gln	Lys	Thr	Gly	Ile	
			245					250						255		
Pro	Glu	Ser	Lys	His	Leu	Gly	Gly	Phe	Pro	Ile	Ser	Gly	Gln	Phe	Leu	
			260					265					270			
Ile	Cys	Thr	Asn	Pro	Asp	Val	Ile	Asn	Glu	His	Asp	Val	Lys	Val	Tyr	
		275				280						285				
Gly	Lys	Glu	Pro	Pro	Gly	Thr	Pro	Pro	Met	Thr	Val	Pro	His	Leu	Asp	
	290					295					300					
Thr	Arg	Tyr	Ile	Asp	Gly	Glu	Arg	Thr	Leu	Leu	Phe	Gly	Pro	Phe	Ala	
305					310					315				320		
Asn	Ile	Gly	Pro	Lys	Phe	Leu	Arg	Asn	Gly	Ser	Asn	Leu	Asp	Leu	Phe	
				325					330					335		
Lys	Ser	Val	Lys	Pro	Tyr	Asn	Ile	Thr	Thr	Leu	Leu	Ala	Ser	Ala	Val	
			340					345						350		

Lys Asn Leu Pro Leu Ile Lys Tyr Ser Ile Asp Gln Val Leu Met Thr
355 360 365

Lys Glu Gly Cys Met Asn His Leu Arg Thr Phe Tyr Pro Glu Ala Arg
370 375 380

Asp Glu Asp Trp Gln Leu Tyr Thr Ala Gly Lys Arg Val Gln Val Ile
385 390 395 400

Lys Asp Thr Lys Glu His Gly Lys Gly Phe Ile Gln Phe Gly Thr Glu
405 410 415

Val Val Asn Ser Lys Asp His Ser Val Ile Ala Leu Leu Gly Glu Ser
420 425 430

Pro Gly Ala Ser Thr Ser Val Ser Val Ala Leu Glu Val Leu Glu Lys
435 440 445

Asn Phe Ala Glu Tyr Glu Lys Asp Trp Thr Pro Lys Leu Gln Lys Met
450 455 460

Ile Pro Ser Tyr Gly Lys Ser Leu Ile Asp Asp Val Lys Leu Met Arg
465 470 475 480

Ala Thr Arg Lys Gln Thr Ser Lys Asp Leu Glu Leu Asn Tyr Tyr Glu
485 490 495

Ser Lys

<210> 59
<211> 516
<212> PRT
<213> Staphylococcus epidermidis

<400> 59

Met Lys Ile Phe Lys Thr Leu Ser Ser Ile Leu Val Thr Ser Val Leu
1 5 10 15

Ser Val Thr Val Ile Pro Ser Thr Phe Ala Ser Thr Glu Ser Thr Ala
20 25 30

Thr Asn Gln Thr Gln Gln Thr Val Leu Phe Asp Asn Ser His Ala Gln
35 40 45

Thr Ala Gly Ala Ala Asp Trp Val Ile Asp Gly Ala Phe Ser Asp Tyr
50 55 60

Ala Asp Ser Met Arg Lys Gln Gly Tyr Gln Val Lys Glu Leu Glu Gly
65 70 75 80

Glu Ser Asn Ile Ser Asp Gln Ser Leu Gln Gln Ala His Val Leu Val
85 90 95

Ile Pro Glu Ala Asn Asn Pro Phe Lys Glu Asn Glu Gln Lys Ala Ile
100 105 110

Ile Asn Phe Val Lys Asn Gly Gly Ser Val Ile Phe Ile Ser Asp His
115 120 125

Tyr Asn Ala Asp Arg Asn Leu Asn Arg Ile Asp Ser Ser Glu Ser Met
130 135 140

Asn Gly Tyr Arg Arg Gly Ala Tyr Glu Asn Met Thr Lys Asp Met Asn
145 150 155 160

Asn Glu Glu Lys Asn Ser Asn Val Met His Asn Val Lys Ser Ser Asp
165 170 175

Trp Leu Ser Gln Asn Phe Gly Val Arg Phe Arg Tyr Asn Ala Leu Gly
180 185 190

Asp Ile Asn Thr Gln Asn Ile Val Ser Ser Lys Asp Ser Phe Gly Ile
195 200 205

Thr Lys Gly Val Gln Ser Val Ser Met His Ala Gly Ser Thr Leu Ala
210 215 220

Ile Thr Asp Pro Asn Lys Ala Lys Gly Ile Ile Tyr Met Pro Glu His
225 230 235 240

Leu Thr His Ser Gln Lys Trp Pro His Ala Val Asp Gln Gly Ile Tyr
245 250 255

Asn Gly Gly Gly Ile Asn Glu Gly Pro Tyr Val Ala Ile Ser Lys Ile
260 265 270

Gly Lys Gly Lys Ala Ala Phe Ile Gly Asp Ser Ser Leu Val Glu Asp
275 280 285

Arg Ser Pro Lys Tyr Leu Arg Glu Asp Asn Gly Lys Pro Lys Lys Thr

290	295	300
Tyr Asp Gly Phe Lys Glu Gln Asp Asn Gly Lys Leu Leu Asn Asn Leu 305 310 315 320		
Thr Thr Trp Leu Gly Lys Lys Glu Ser Gln Ser Ser Met Lys Asp Met 325 330 335		
Gly Ile Lys Leu Asp Asn Lys Thr Pro Leu Leu Asn Phe Glu Gln Pro 340 345 350		
Glu Asn Ser Ile Glu Pro Gln Lys Glu Pro Trp Thr Asn Pro Ile Glu 355 360 365		
Gly Tyr Lys Trp Tyr Asp Arg Ser Thr Phe Lys Thr Gly Ser Tyr Gly 370 375 380		
Ser Asn Gln Arg Gly Ala Asp Asp Gly Val Asp Asp Lys Ser Ser Ser 385 390 395 400		
His Gln Asn Gln Asn Ala Lys Val Glu Leu Thr Leu Pro Gln Asn Ile 405 410 415		
Gln Pro His His Pro Phe Gln Phe Thr Ile Lys Leu Thr Gly Tyr Glu 420 425 430		
Pro Asn Ser Thr Ile Ser Asp Val Arg Val Gly Leu Tyr Lys Asp Gly 435 440 445		
Gly Lys Gln Ile Gly Ser Phe Ser Ser Asn Arg Asn Gln Phe Asn Thr 450 455 460		
Leu Gly Tyr Ser Pro Gly Gln Ser Ile Lys Ala Asn Gly Ala Gly Glu 465 470 475 480		
Ala Ser Phe Thr Leu Thr Ala Lys Val Thr Asp Glu Ile Lys Asp Ala 485 490 495		
Asn Ile Arg Val Lys Gln Gly Lys Lys Ile Leu Leu Thr Gln Lys Met 500 505 510		
Asn Glu Asn Phe 515		

<210> 60

<211> 84

<212> PRT

<213> Staphylococcus epidermidis

<400> 60

Gly Thr Pro Leu Glu Leu Val Phe Val Asn Thr Leu Gly Pro Lys Pro
1 5 10 15

Cys Phe Ala Lys Pro Asn Lys Ile Leu Leu Leu Glu Tyr Ile Pro Leu
20 25 30

Phe Val Ala Asp Ala Ala Ala Val Lys Thr Thr Lys Leu Thr Met Pro
35 40 45

Ala Ala Lys Gly Thr Pro Ile Ser Val Asn Asn Leu Thr Asn Gly Leu
50 55 60

Leu Ser Gly Ser Thr Leu Asn His Gly Met Thr Asp Met Ile Thr Ser
65 70 75 80

Lys Pro Pro Ile

<210> 61

<211> 54

<212> PRT

<213> Staphylococcus epidermidis

<400> 61

Ser Ser Leu Ser Thr Ile Ile Pro Phe Ser Leu Gly Ala Leu Gly Lys
1 5 10 15

Phe Asn Ser Phe Ile Glu Gln Ile Ile Pro Leu Glu Ser Thr Pro Arg
20 25 30

Asn Trp Ala Ser Leu Ile Thr Ile Pro Leu Gly Ile Thr Ala Pro Thr
35 40 45

Phe Ala Thr Thr Thr Phe
50

<210> 62

<211> 116

<212> PRT

<213> Staphylococcus aureus

<400> 62

Met Lys Phe Lys Lys Tyr Ile Leu Thr Gly Thr Leu Ala Leu Leu Leu
1 5 10 15

Ser Ser Thr Gly Ile Ala Thr Ile Glu Gly Asn Lys Ala Asp Ala Ser
20 25 30

Ser Leu Asp Lys Tyr Leu Thr Glu Ser Gln Phe His Asp Lys Arg Ile
35 40 45

Ala Glu Glu Leu Arg Thr Leu Leu Asn Lys Ser Asn Val Tyr Ala Leu
50 55 60

Ala Ala Gly Ser Leu Asn Pro Tyr Tyr Lys Arg Thr Ile Met Met Asn
65 70 75 80

Glu Tyr Arg Ala Lys Ala Ala Leu Lys Lys Asn Asp Phe Val Ser Met
85 90 95

Ala Asp Ala Lys Val Ala Leu Glu Lys Ile Tyr Lys Glu Ile Asp Glu
100 105 110

Ile Ile Asn Arg
115

<210> 63
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Peptide

<400> 63
Lys Leu Lys Leu Leu Leu Leu Leu Lys Leu Lys
1 5 10

<210> 64
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Peptide

<400> 64
Arg Leu Ala Gly Leu Leu Arg Lys Gly Gly Glu Lys Ile Gly Glu Lys
1 5 10 15

Leu Lys Lys Ile Gly Gln Lys Ile Lys Asn Phe Phe Gln Lys Leu Val
20 25 30

Pro Gln Pro Glu
35